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Characterization and Amplification of Retrotransposable Elements Platy-1 and Alu in the Cebidae Lineage of Platyrrhine Primates

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CHARACTERIZATION AND AMPLIFICATION OF RETROTRANSPOSABLE ELEMENTS PLATY-1 AND ALU IN THE CEBIDAE LINEAGE OF PLATYRRHINE PRIMATES

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List of Abbreviations

TE	transposable element
LTR	long terminal repeat
LINE	long INterspersed element
TPRT	target primed reverse transcription
ORF	open reading frame
RT	reverse transcriptase
EN	endonuclease
TSD	target site duplications
SINE	short interspersed element
mya	million years ago
my	million years
PCR	polymerase chain reaction
SNP	single nucleotide polymorphism
NWM	New World monkeys
OWM	Old World monkeys
ILS	incomplete lineage sorting
RI	retention index
CI	consistency index
HI	homoplasy index
SRA	sequence read archive

Abstract

Alu mobile elements are much more than "junk DNA". Inherent properties such as high copy number, small ~300 bp size, and their nearly homoplasy-free nature make these elements particularly useful in resolving primate phylogenies. In addition, shared sequence features and identity with the *Alu* element allow for discovery of new SINE retrotransposons, such as the Platyrrhine-limited Platy-1 element. Building on previous research of subfamily analysis, the Platy-1 and *Alu* elements can be used not only to explore the controversial New World monkey (NWM) phylogeny, but also the mode and tempo of their amplification in different primate genera and species.

Chapter 2 explores the amplification of the NWM-limited Platy-1 element. While a large expansion of Platy-1 elements was observed in the marmoset genome, the same cannot be said for the capuchin monkey, squirrel monkey and owl monkey genomes. Of these three genomes, only the owl monkey genome contained evidence of Platy-1 mobilization as shown by the presence of polymorphic (for insertion presence/absence) Platy-1 insertions, low percent divergence values, and the emergence of two new Platy-1 subfamilies. However, there were too few phylogenetically informative Platy-1 insertions to resolve the controversial Cebidae NWM phylogeny.

Chapter 3 characterizes the use of the polyDetect pipeline mapping short sequence reads to a reference genome for detecting shared *Alu* elements that could resolve the NWM phylogeny. However, the short homology provided by the reads was not enough to accurately predict shared *Alu* insertions of these four NWM genera that have diverged by ~20 million years.

Chapter 4 explores not only using longer stretches of identity/homology in the hope of accurately detecting shared *Alu* insertions, but also analyzes *Alu* subfamily evolution to resolve

the Cebidae NWM phylogeny. A largely congruent network analysis and Bayesian phylogenetic tree were generated as well as *Alu* alignments, all suggesting that the branching pattern of marmoset, owl monkey, squirrel monkey and capuchin monkey starts with marmoset as the most basal of these four Cebidae NWMs, with owl monkey as a sister outgroup to the sister group of squirrel monkey and capuchin monkey.

Chapter 1. Introduction and Background

Introduction

Transposable elements (TEs) were first discovered by Barbara McClintock after her observations of "mutable loci" and their influence on maize kernel color (McClintock 1950). McClintock categorized two types of mutable elements: those that depended upon a separate factor in order to make them mutable and another that was autonomous in terms of its mutability, a.k.a., non-autonomous and autonomous TEs. McClintock also observed that the phenotypic changes resulting from these mutational events were reminiscent of those caused by substances that cause chromosomal breakage, such as ultraviolet light, suggesting that these mutable loci could cause chromosomal breakage. In addition, she identified families of TEs that could not interact with one another (McClintock 1950), indicating that there were distinct and different types of TEs.

Major division of TEs

Although McClintock correctly identified autonomous and non-autonomous elements and different families of elements, those families had yet to be meticulously characterized. A major division of TEs lies in their movement mechanism via a DNA (DNA TEs) or RNA (retrotransposable elements) intermediate (Cordaux and Batzer 2009). While DNA TEs are essentially no longer active in mammalian genomes (Feschotte and Pritham 2007), with the notable exception of bats (Ray et al. 2008), retrotransposable elements, autonomous and non-autonomous, are actively mobilizing (Brouha et al. 2003; Han et al. 2005; Mills et al. 2006; Baker et al. 2018). Retrotransposable elements can be broadly categorized into those elements that have long terminal repeats (LTR) and those not that do not (non-LTR). Autonomous non-LTR elements include long interspersed (LINE) elements (Deininger and Batzer 2002; Konkel et

al. 2010). These elements contain the coding capacity necessary for retrotransposition via target primed reversed transcription (TPRT) (Luan et al. 1993). One active LINE element in primates is L1. The ~6000 bp L1 encodes two major proteins from two open reading frames (ORF), ORF1 and ORF2 that encode proteins ORF1p and ORF2p, respectively. ORF1p has nucleic acid chaperone functions while ORF2p has both reverse transcriptase (RT) and endonuclease functions (EN) (Feng et al. 1996; Moran et al. 1996). Although L1 elements make up 10% of the human genome by mass (Lander et al. 2001), only a handful of these TEs are capable of movement (Brouha et al. 2003).

Target primed reverse transcription (TPRT)

TPRT begins with the L1 ORF2p EN targeting the sequence 5'-TT|AAAA 3', where the vertical line represents the cut site on the bottom strand of the DNA. The A-rich tail or the polyA tail base pairs with the free poly T sequence (Luan et al. 1993; Morrish et al. 2002). The free 3'-OH group on the bottom strand, generated during the cut by ORF2p EN, primes reverse transcription of the L1 or *Alu* RNA by the ORF2p RT (Dewannieux et al. 2003). This is followed by a staggered second strand cleavage and subsequent integration of the transposable element cDNA and the subsequent removal of RNA and the completion of the second strand synthesis. This process generates target site duplications (TSDs). Therefore, elements that move via TPRT will have the following characteristics: a 3' A-rich tail, TSDs, and an RNA intermediate. This process can be verified for putative elements using a cell-based assay (Moran et al. 1996) or by an analysis of the aforementioned DNA sequence characteristics.

***Alu* mobile elements**

Alu mobile elements are examples of non-autonomous short interspersed elements (SINE) specific to primates (Houck et al. 1979). These elements comprise at least 17% of the

human genome (Lander et al. 2001) and are the most successful transposable element in terms of copy number with 1.1 million copies in most primate genomes (Lander et al. 2001; Baker et al. 2017). *Alu* elements are short, ~300 bp, with a dimeric structure (Batzer and Deininger 2002; Deininger and Batzer 2002; Konkel et al. 2010; Deininger 2011). The left monomer contains the A and B boxes necessary for RNA polymerase III transcription to generate the RNA intermediate characteristic of retrotransposable elements (Dieci et al. 2013). The left and right monomers are separated by an A-rich region. The *Alu* element 3' end is comprised of an A-rich tail (Batzer and Deininger 2002; Deininger and Batzer 2002; Deininger 2011). The entire element is surrounded on both the 5' and 3' ends by target site duplications (TSDs) as a product of movement via TPRT (Deininger and Batzer 2002; Cordaux and Batzer 2009; Konkel et al. 2010). Their movement relies on internal and external factors. External factors include the availability of L1 protein ORF2p but not ORF1p (Wallace et al. 2008). Therefore, even though many L1 elements are truncated on their 5' end (Szak et al. 2002), they may still be able to express the ORF2p protein allowing for *Alu* mobilization.

Intrinsic factors necessary for *Alu* mobilization include the length and homogeneity of the 3' A-rich tail (Dewannieux and Heidmann 2005), integrity of the A and B boxes for transcription, RNA structure and proximity of the RNA polymerase III termination sequence to the 3' end of the element (Goodier and Maraia 1998). In addition, the upstream sequence may also play a role in fostering *Alu* transcription (Roy et al. 2000). *Alu* elements have evolved from 7SL RNA, a component of the signal recognition particle (SRP), a protein-RNA complex involved in targeting specific proteins to the endoplasmic reticulum or plasma membrane in eukaryotes and prokaryotes, respectively. (Ullu and Tschudi 1984; Labuda and Zietkiewicz 1994). Each monomer of the dimeric *Alu* structure maintains the folding structure of 7SL RNA,

allowing *Alu* RNA to bind SRP9/14 (Bovia et al. 1997; Bennett et al. 2008; Berger et al. 2014). It is thought that SRP9/14 binding facilitates *Alu* mobilization by bringing *Alu* RNA near active ribosomes and L1 machinery (Bennett et al. 2008). This RNA binding function of SRP9/14 could potentially mitigate the need for L1 ORF1p (Dewannieux et al. 2003). The 3' homogeneous A-rich tail is not only an indicator of element age, but also important for binding polyA binding protein (PABP) (Boeke 1997; Dai et al. 2012). This interaction could also facilitate the mobilization of *Alu* elements via a similar mechanism as binding SRP9/14.

Platy-1 retrotransposable elements

Like *Alu,* Platy-1 elements are short SINE elements only found in the primate order. In addition, Platy-1 elements have TSDs and an A-rich tail indicating that both *Alu* elements and Platy-1 elements move via TPRT. Conserved A and B boxes in the 5' end of the Platy-1 element also suggest that it is transcribed by RNA polymerase III (Konkel et al. 2016). However, unlike *Alu* elements, Platy-1 elements are only ~100 bp in length and are limited to the parvorder Platyrrhine, or New World monkeys (NWM) within the primate order (Konkel et al. 2016). Platy-1 limitation to NWM suggests that they are a younger family of repeat elements compared to *Alu*. An alignment of the Platy-1 sequence to *Alu* sequences demonstrates that they are derived from 7SL RNA and evolved from an *Alu.* Platy-1 elements were first discovered in the common marmoset (*Callithrix jacchus*), with ~2200 full-length elements representing 62 Platy-1 subfamilies reported (Konkel et al. 2016). In addition, 10% of these elements were an exact match to their corresponding consensus sequence (Konkel et al. 2016). As the percent divergence increases so does the associated age of the element insertion. Therefore, there is evidence of recent Platy-1 insertions in marmoset. However, marmoset was the only NWM genome analyzed for Platy-1 content in the initial study (Konkel et al. 2016).

Evolution of *Alu* elements in primates

Alu elements can be broadly categorized into three groups. The oldest subfamily, *Alu*J, can be found in all primate lineages, suggesting early mobilization prior to speciation roughly 65 million years ago (mya) (Deininger and Daniels 1986). The second oldest subfamily, *Alu*S, was active after the separation of Strepsirrhines and Tarsiformes from Platyrrhines and Catarrhines (Jurka and Smith 1988; Kapitonov and Jurka 1996; Konkel et al. 2010). Strepsirrhines, or "wet-nosed" primates, consist of lemurs, galagos and lorises while Tarsiformes consist of tarsiers (Vaughan 2000). Platyrrhines are found in the Americas and Catarrhines, or Old World monkeys (OWM), are found in Africa, India and Asia (Vaughan 2000). The youngest subfamily, *Alu*Y, is found only in Catarrhines (Batzer and Deininger 1991; Batzer et al. 1991; Batzer et al. 1994; Konkel et al. 2010). Parallel activity of *Alu* subfamilies can occur in different primate species with the rise of new *Alu* subfamilies in any given lineage. Due to this parallel evolution, each lineage of the primate order contains its own unique set of *Alu* mobile elements. New *Alu* subfamilies occur via the stepwise accumulation of diagnostic mutations (Slagel et al. 1987; Jurka and Smith 1988).

New World monkeys

New World monkeys (NWM), or Platyrrhines, split from OWM, or Catarrhines, roughly ~35 million years ago and inhabit the tropical forests of Mexico and Central and South America (Perez et al. 2013). Although the mode of travel to the New World is unknown, these primates are thought to have evolved from an African ancestor (Bond et al. 2015). The term Platyrrhine refers to their sideways facing nostrils, in contrast to Catarrhines which have downward facing nostrils (Vaughan 2000). NWM also differ from OWM in terms of body size and the generally arboreal niche they inhabit (Hershkovitz 1977; Marroig and Cheverud 2005; Ward and Vallender

2012; Perez et al. 2013). In addition, species within NWM have a wide variety of unstudied behavioral and morphological characteristics. Thus, the knowledge of the behavior of NWM compared to OWM is less comprehensive. In addition, the harsh conditions in South America, and in particular the Amazonian region, do not foster ideal conditions for fossil formation. This, in combination with lack of behavioral knowledge, creates a circumstance where the phylogeny of NWM has been highly contentious. An initial analysis of NWM cranial morphology and presumed important speciation characteristics in 1977 by Hershkovitz led to a phylogeny with three families: 1) Callitrichidae, containing four genera, which included tamarins and marmosets; 2) the monotypic Callimiconidae, containing the genus *Callimico*, and 3) Cebidae, containing eleven genera, which included all other NWM types, including capuchin monkeys, owl monkeys, squirrel monkeys, and monkeys that now belong to different NWM families, such as those belonging to the *Pithecia* and *Brachyteles* genera. While this classification was undisputed for a long period of time, it ignored the more difficult placements that include the genera *Cebus*, *Aotus*, and *Saimiri* (Hershkovitz 1977). It was not until molecular markers were utilized, instead of morphology, that a consensus was reached on the three NWM families: Cebidae (containing the *Cebus*, *Aotus*, *Saimiri* genera and the Callitrichidae), Atelidae and Pitheciidae (Schneider and Sampaio 2015). However, there is not a consensus as to the inter-generic relationships within each family. For example, the position of the *Aotus* genus within Cebidae remains controversial. Although there are shared *Alu* mobile element markers that place *Aotus* squarely within the Cebidae family (Ray and Batzer 2005; Osterholz et al. 2009), there is conflicting information as to the position of *Aotus* in the Cebidae lineage (Osterholz et al. 2009). This ambiguity is due to the rapid 1-2 my speciation event(s) leading to the separation of the Cebidae families that could produce incomplete lineage sorting events. Incomplete lineage sorting (ILS) is a homoplasic

event that occurs if at the time of speciation there is a polymorphic insertion in the population (Nei 1987; Pamilo and Nei 1988; Ray et al 2006). ILS creates a situation where the gene relationships are different from the species relationships. In addition, the NWM rapid speciation occurred 19-20 mya (Schneider 2000; Perelman et al. 2011). This contrasts with other species with rapid, yet recent, radiation events such as the baboon, or genus *Papio*. There is current admixture and incomplete lineage sorting that occurs within the *Papio* lineage (Rogers et al 2019). However, this change is on-going and can be parsed out by using larger sample sizes of modern-day baboons (Jordan et al. 2018). This is not the case with NWM. Therefore, careful consideration and thorough analysis must supplement any phylogenetic tree produced by any means for NWM.

Utilities of TEs

Alu elements present researchers with a unique phylogenetic marker. *Alu* elements are nearly homoplasy-free markers with a known ancestral state of the absence of the insertion (Ray et al. 2006; Hillis 1999; Perna et al. 1992; Batzer et al. 1991; Batzer et al. 1994). In addition, these short elements are easily analyzed via polymerase chain reaction (PCR) and subsequent gel electrophoresis analysis (Perna et al. 1992). *Alu* elements contrast with other phylogenetic markers such as single nucleotide polymorphisms (SNPs) or DNA sequence data in which multiple mutations can obscure phylogenetic signal. In addition, SNPs are identical by state, not necessarily by descent. Furthermore, sequencing, in comparison to PCR, is required to analyze SNPs. There are no known mechanisms for the precise excision of an *Alu* element. In addition, near-parallel and precise-parallel insertions are rare (Ray et al. 2006). While older *Alu* elements that are fixed in a population are phylogenetically informative, younger insertions are informative for population genetics (Bamshad et al. 2003; Watkins et al. 2003; Stewart et al.

2011; Steely et al. 2017; Baker et al. 2018). *Alu* insertions have proven instrumental in the resolution of many phylogenies in primates (Singer et al. 2003; Roos et al. 2004; Ray and Batzer 2005; Ray et al. 2005; Li et al. 2009; McLain et al. 2012; Meyer et al. 2012; Jordan et al. 2018). In addition, the amplification dynamics of TEs within and among genomes can highlight differences between species such as effective population size, and possible environmental or genomic differences.

The Era of Big Data

Since the advent of high-throughput sequencing techniques, many more genomes have been sequenced, such that approximately every seven months the amount of genomic information available doubles (Stephens et al. 2015). With this massive amount of data there necessarily comes a need for new methods to process said data. Most sequencing data comes in short read format, although the number of fully assembled, high quality genomes is increasing (Stephens et al. 2015). Due to the nature of short reads produced from sequencing platforms such as Illumina, there is a limitation as to how much information can be gleaned from short reads alone. In addition, depending upon the size of the TE, they may be underrepresented in short read data. It is therefore crucial to complement these analyses with wet bench experiments or alternative methods.

Chapter 2 of this thesis explores the amplification dynamics of a newly discovered retrotransposable element, Platy-1, in three NWM genomes, owl monkey (*Aotus nancymaae*), squirrel monkey (*Saimiri boliviensis*) and capuchin monkey (*Cebus imitator*), to add to the information already ascertained from the common marmoset genome (*Callithrix jacchus*). Compared to the ~2200 full length Platy-1 elements found in the marmoset genome, a fraction of this number was discovered in owl monkey, squirrel monkey and capuchin monkey genomes. In

addition, in comparison to the 62 subfamilies present in the marmoset genome, only 6 or 7 Platy-1 subfamilies were found in the other three NWM genomes studied. When the lineage-specific elements were assessed, all elements were fixed in the squirrel monkey and capuchin monkey genomes, with intermediate to large divergences for full-length Platy-1 elements. The fixed Platy-1 elements and large divergence values indicate that these elements have little recent activity in these two genomes. However, a higher number of lineage specific elements were observed in the owl monkey genome, with 26% of PCR-analyzed Platy-1 loci polymorphic in the owl monkey population. In addition, the full-length elements ascertained from the owl monkey genome had divergence values indicating younger to intermediate ages, with two new subfamilies identified. The polymorphic insertions, low divergence values, and formation of new subfamilies indicate that Platy-1 mobilization is on-going in the owl monkey genome. However, the marmoset genome displayed much higher levels of Platy-1 element activity in comparison to the owl monkey, squirrel monkey and capuchin monkey genomes.

Chapter 3 explores a computational method to elucidate the NWM phylogeny within Cebidae. Following a thorough analysis of the polyDetect computational pipeline when applied to the NWM phylogeny it was determined that the limited homology of the short read data obscured the accurate identification of shared *Alu* insertions by four different NWM representing four genera diverged by ~20 my. A possible homology problem leading to inaccuracies in the polyDetect output was evident by the conflict of the polyDetect output and the corresponding extracted and aligned sequences from the assembled genomes. In addition, the output of this pipeline was greatly influenced by the reference genome used to map the reads, producing conflicting phylogenetic trees, all with high bootstrap support. Although this pipeline is sufficient for closely-related data sets, resolving the NWM phylogeny, with emphasis on the

placement of the *Aotus* genus within the Cebidae lineage, requires longer stretches of assembled sequences if a homology-based assessment is to be performed.

Chapter 4 makes use of an alternative alignment method to the polyDetect computational piopeline to resolve the NWM phylogeny within Cebidae. Briefly, this method involved extracting full-length *Alu* elements with flanking sequence from four NWM genomes (marmoset, owl monkey, squirrel monkey and capuchin monkey) and using BLAT (Kent 2002) followed by MUSCLE (Edgar 2004) alignment and subsequent gap presence/absence analysis using a custom python script to parse the insertions into different categories depending upon which NWM genomes shared the presence of insertion. To complement these analyses, an assessment of the evolution of *Alu* subfamilies in NWM genomes was completed. The subfamily analysis was achieved by compiling prior network analyses of lineage-specific *Alu* subfamilies in the marmoset (Worley et al. 2014) and squirrel monkey (Baker et al. 2017) genomes and adding lineage-specific *Alu* subfamilies from the capuchin monkey and owl monkey genomes. These combined sequences were aligned with *Alu* subfamilies obtained from RepBase (Jurka et al. 2005) and Ray et al. (2005). In addition to a network, a Bayesian phylogenetic tree was also constructed. The combination of the *Alu* alignments, network and Bayesian tree pointed toward a branching pattern where capuchin monkey and squirrel monkey are sister groups, with owl monkey as an outgroup to these sister groups. Marmoset appears to be the most basal of the four NWM in this study, acting as a sister group to the capuchin monkey, squirrel monkey and owl monkey group.

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Chapter 2. Amplification Dynamics of Platy-1 Retrotransposons in the Cebidae Platyrrhine Lineage

Introduction

Transposable elements (TEs) are discrete pieces of DNA that are able to move from one genomic location to another. These elements can be broadly categorized based on their movement mechanism, either "cut-and-paste" or "copy-and-paste". The former category includes DNA transposable elements that mobilize via a DNA intermediate. (Hellen and Brookfield 2013). The latter category includes retrotransposable elements that move via an RNA intermediate (Batzer and Deininger 2002; Konkel et al. 2010). In primates, retrotransposable non-autonomous short interspersed elements (SINEs) such as *Alu* elements (Houck et al. 1979) and autonomous long interspersed elements (LINEs) called L1s make up roughly 10% and 17% of the genome by mass, respectively (Lander et al. 2001; Batzer and Deininger 2002; Richardson et al. 2015). The high copy number *Alu* elements are ~300 base pairs (bp) long with a dimeric structure, separated by a middle A-rich region. These elements are derived from the 7SL RNA, a component of the signal recognition particle (Batzer and Deininger 2002; Konkel et al. 2010). These elements are mobilized via a retrotransposition mechanism called target-primed reverse transcription (TPRT) (Luan et al. 1993; Morrish et al. 2002). However, *Alu* does not code for the proteins required for TPRT and must rely on the protein products of L1s for movement (Dewannieux et al. 2003). Hallmarks of TPRT include a 5' and 3' flanking target site duplication (TSD), endonuclease cleavage site and a 3' A-rich tail, allowing for additional elements that mobilize via this mechanism to be identified (Morrish et al. 2002). The manner of *Alu*

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mobilization generates random and non-random mutations. The non-random mutations are termed diagnostic mutations and serve to divide *Alu* repeats into subfamilies (Jurka and Smith 1988; Deininger et al. 1992). The independent amplification of *Alu* repeats that occurs in separate lineages may lead to the propagation of new mobile element subfamilies.

New World monkeys (NWM) are a diverse group of primates belonging to the parvorder Platyrrhini. These small to mid-sized primates are located in Central and South America and belong to one of three families: Cebidae (small, arboreal monkeys), Atelidae (large monkeys with prehensile tails), or Pitheciidae (herbivorous monkeys) (Schneider and Sampaio 2015). Since the first study of NWM cladistics, the phylogeny of NWM has been under debate (Ray and Batzer 2005; Ray et al. 2005; Osterholz et al. 2009). This is in part due to poor fossil records (Perez et al. 2013) making divergence times and speciation events difficult to pinpoint. In addition, different morphological and molecular markers have produced conflicting results for some portions of the NWM tree (Dumas et al. 2007; Pacheco et al. 2010; de Oliveira et al. 2012; Hiroshige et al. 2015; Capozzi et al. 2016). However, there is general agreement of the three NWM families as well as the genera included. Within the Cebidae family, there are three clades whose phylogenetic relationship is still being studied: *Aotinae, Cebinae,* and *Callitrichinae* (Schneider and Sampaio 2015). *Aotinae* includes night monkeys, belonging to the *Aotus* genus, *Cebinae* includes the extant genus *Saimiri* and capuchin monkeys which include two extant genera, *Cebus* and *Sapajus* (formerly subsumed into one genus, *Cebus*) (Alfaro et al. 2012), and *Callitrichinae* which includes marmosets (genera *Callithrix, Callimico, Cebuella and Mico)* and tamarins (genera *Leontopithecus* and *Saguinus*) (Garbino and Martins-Junior 2018). While reported divergence times and radiation of these three clades have varied, there is a general consensus that the rapid radiation occurred over a short time of 1-2 million years. Estimates of

when this divergence occurred range from 19.25 mya (Perelman et al. 2011) to 23.2 mya (Schneider 2000).

Recently, a new retrotransposable element was discovered in the common marmoset genome and subsequently found to be specific to the Platyrrhini parvorder. Deemed, "Platy-1", these ~100 bp elements have the hallmarks of movement via TPRT (Konkel et al. 2016). In addition, these elements share some structure and sequence similarity with *Alu* elements, a primate-specific SINE, suggesting that Platy-1 likely originated from an *Alu* element and is 7SL RNA derived (Konkel et al. 2016). Roughly 2200 Platy-1 elements were found in the common marmoset genome [calJac3], prompting a closer look at other NWMs with whole genome sequence data available.

Although once thought to be "junk" DNA (Kazazian 2011), TEs have had an unexpected influence on primate biology in terms of disease, phenotypes and evolution. TEs can cause genomic instability via double-stranded breaks (Belgnaoui et al. 2006; Gasior et al. 2006) and non-homologous recombination (Han et al. 2005a; Startek et al. 2015), potentially influencing meiosis, depending upon the location of the insertion as well as resulting in the contraction or expansion of genome size. In addition, based on their insertional location, TEs can affect transcriptional control via influencing alternative splicing if inserted into the coding region of a gene, disrupting the formation of a gene product, or influencing the methylation status of the TE's surrounding environment (Cordaux and Batzer 2009). It is therefore informative to understand the amplification dynamics of mobile elements in order to understand how genomes have evolved, particularly because of parallel evolution in which many mobile elements may be active in multiple lineages simultaneously. Due to parallel evolution, each NWM lineage will have its' own unique distribution of not only TE families, but also distinctive subfamilies within

each family. For example, the discovery of 46 *Saimiri* lineage-specific *Alu* subfamilies was recently reported (Baker et al. 2017), most of which derived from the larger group of established *Alu*Ta subfamilies. *Alu*Ta subfamilies are specific to NWM as the result of a unique fusion event between two anthropoid *Alu*S subfamilies (Ray and Batzer 2005) and have been used to study phylogenetic relationships.

The purpose of this study was to characterize the Platy-1 elements found in the current genome assemblies of other Platyrrhine primates in order to determine the quantity of Platy-1 elements as well as the amplification dynamics in comparison to the common marmoset genome (Konkel et al. 2016).

Materials and Methods

Platy-1 Lineage Specificity

The capuchin monkey (*Cebus imitator*), owl monkey (*Aotus nancymaae*) and squirrel monkey (*Saimiri boliviensis*) genomes were obtained from NCBI (cebus-Cebus_imitator-1.0; owl-Anan_1.0) and the University of California Santa Cruz (UCSC) genome browser (squirrel-saiBol1). Assembly statistics for each genome are available in Table 2.1 and representative

Table 2.1. Genome assembly statistics. The assembly statistics for the NWM genomes used in this study are shown below

Genome	Common name	Assembly	N50 (Contig)	N50 (Scaffold)	Coverage	Number of gaps	Size (bp)
Cebus imitator	Capuchin monkey	Cebus_imitator-1.0	41,196	5,274,112	81x	133,441	2.72×10^9
Saimiri boliviensis	Squirrel monkey	saiBol1	38,823	18,744,880	80x	148,728	2.61×10^9
Aotus nancymaae	Owl monkey	Anan_1.0	28,503	8,280,397	113.4x	215,259	2.93×10^9

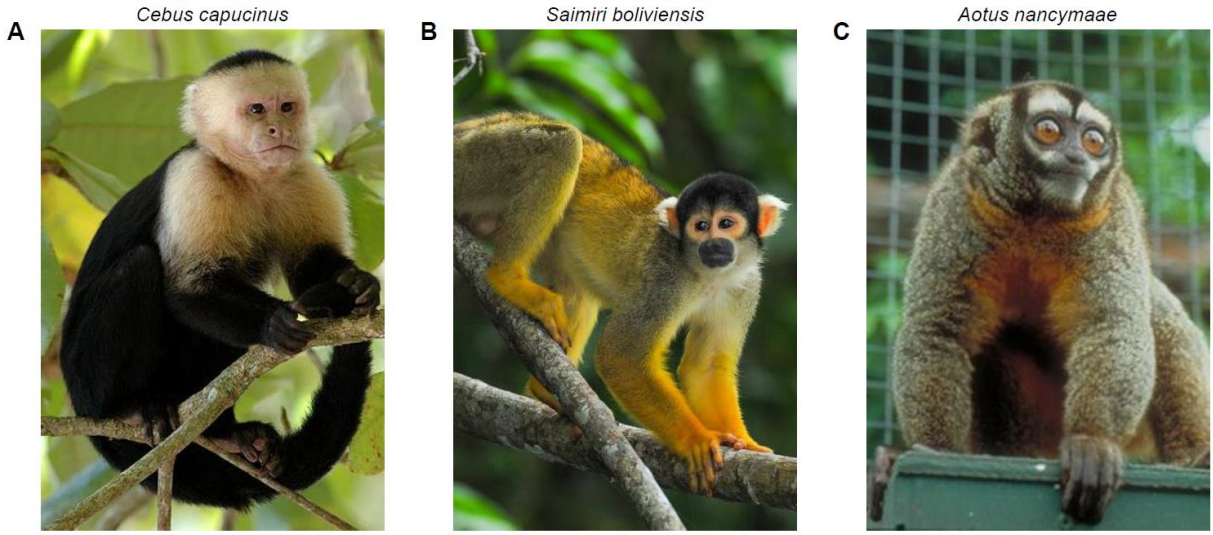


Figure 2.1. Photographs representative of the NWM used in this study. A) *Cebus capucinus* or capuchin monkey; B) *Saimiri boliviensis* or squirrel monkey; C) *Aotus nancymaae* or owl monkey (Cawthon Lang 2005).

photographs for each species are shown in Figure 2.1). These genomes were analyzed for Platy-1 elements using RepeatMasker (RepeatMasker-Open-4.0) utilizing a custom library of the 62 Platy-1 subfamilies previously defined (Konkel et al. 2016) and all current *Alu* subfamily consensus sequences obtained from RepBase (Jurka et al. 2005). Full-length Platy-1 elements were defined as possessing a start position no less than 4 bp and an end position not shorter than two nucleotides prior to the A-tail within the consensus sequence (Konkel et al. 2016). Full-length elements were extracted from the RepeatMasker output using a custom python script. These elements, along with 600 bp of flanking sequence on both the 5' and the 3' ends of the Platy-1 insertion, were compared to the common marmoset (*Callithrix jacchus*; /calJac3) and the remaining NWM genomes using a locally installed version of BLAT (Kent 2002) to determine lineage specificity. Specificity was determined by visualizing the BLAT alignments using pslPretty and observing a ~100 bp gap. For each locus an alignment file was generated in BioEdit (Hall 1999) to be used for the design of oligonucleotide primers.

Platy-1 Shared Elements

To analyze shared elements among NWM, the whole-genome aligner mugsy (Angiuoli and Salzberg 2011) was utilized. All Platy-1 elements with flanking sequence for each lineage (squirrel, capuchin and owl monkeys as well as marmoset) were put into one FASTA file. The resulting four FASTA files were then aligned as if they were whole genomes using the whole genome function in mugsy. The output .maf file was visualized using GMAJ (globin.bx.psu.edu/dist/gmaj/) and manually assessed for alignment precision. This analysis proved fruitful for obtaining elements that were shared among all four of the genomes analyzed. However, elements that were computationally predicted to be shared between only two or three of the four genomes, typically had gaps in the sequence assembly of the genome(s) in which the insertion was absent, thus obscuring any potential phylogenetically informative data. To overcome this limitation, for the pool of elements not shared among all four genomes we used BLAT followed by a custom python script to obtain orthologous sequences from each genome and then aligned all four sequences for each locus using BioEdit (Hall 1999).

Oligonucleotide Primer Design

The loci determined to contain Platy-1 elements unique to each NWM were put into individual files containing the orthologous sequences from marmoset, squirrel monkey, owl monkey and capuchin monkey genomes. These sequences were aligned using CLUSTALW (Thompson et al. 1994) and/or MUSCLE (Edgar 2004). Forward and reverse oligonucleotide primers for polymerase chain reaction (PCR) were designed using Primer3 (v.0.4.0) and checked in BioEdit to ensure minimal mismatches to allow for the amplification of a PCR product in all genomes specified. In silico PCR was used to confirm the oligonucleotide

primers would amplify only one product in multiple species. The same process was followed for the shared Platy-1 elements (Table A2.1, Table A2.2, Table A2.3).

DNA Samples

DNA samples are described in Table A2.5, Table A2.6, Table A2.7, and Table A2.8. Briefly, there were four panels utilized for this study: a NWM panel (Table A2.5), a squirrel monkey panel (Table A2.7), an owl monkey panel (Table A2.8), and a capuchin monkey panel (Table A2.6). The NWM panel contained three Old World monkeys (OWM) and sixteen NWM species representing the three NWM families. This DNA panel was used to screen elements for lineage-specificity. The squirrel monkey panel included DNA samples from 32 individuals of the genus *Saimiri* representing five species, the owl monkey panel included DNA samples from 23 individuals of the genus *Aotus* representing five species, and the capuchin monkey panel included DNA from 14 different capuchin monkeys, 8 *Cebus apella*, now considered genus *Sapajus apella* (Alfaro et al. 2012), and 6 individuals from genus *Cebus* including the *Cebus imitator* sample used as the reference genome.

Polymerase Chain Reaction (PCR) Amplification

PCR amplification was performed in 25 µL reactions containing 25 µg of template DNA, 200 nM of each primer, 1.5 mM $MgCl_2$, 10x PCR buffer (1x: 50 mM KCl; 10 mM TrisHCl, pH 8.4), 0.2 mM dNTPs, and 1 unit of *Taq* DNA polymerase. The PCR reaction protocol is as follows: 94°C for 1 min, 32 cycles of denaturation at 94°C for 30 s, 30 s at the appropriate annealing temperature (typically 57ºC), extension at 72°C for 30 s, followed by a final 72°C extension step for 2 min. Gel electrophoresis was performed on a 2% agarose gel containing 0.2 µg/mL ethidium bromide for 60 min at 180 V. UV fluorescence was used to visualize the DNA fragments using a BioRad ChemiDoc XRS imaging system (Hercules, CA). If PCR results were

weak or unresolved, the PCR reaction was repeated using hot-start with the JumpStart *Taq* DNA polymerase kit (Sigma Aldrich). Genotypes were recorded in a Microsoft Excel worksheet as (0,0) homozygous absent, (1,1) homozygous present or (1,0) for heterozygous (Table A2.9, Table A2.10, Table A2.11).

Age of Platy-1 elements

The age of the Platy-1 elements was estimated by utilizing the percent divergence of each element to the subfamily consensus sequence, a feature available in the RepeatMasker output. The mutation rate of 0.006024 per base per million years (my) (Konkel et al. 2016) was used to estimate the age of the Platy-1 subfamilies. This rate is the composite of the substitution rate of the crown Platyrrhines and the crown Cebidae (Perez et al. 2013; Konkel et al. 2016). This mutation rate, along with the equation:

$$T = D/t$$

where *D* is the percent divergence and *t* is the substitution rate, was used to calculate the age (T) (my) of the Platy-1 elements (Table A1.12, Table A2.13, Table A2.14).

Results

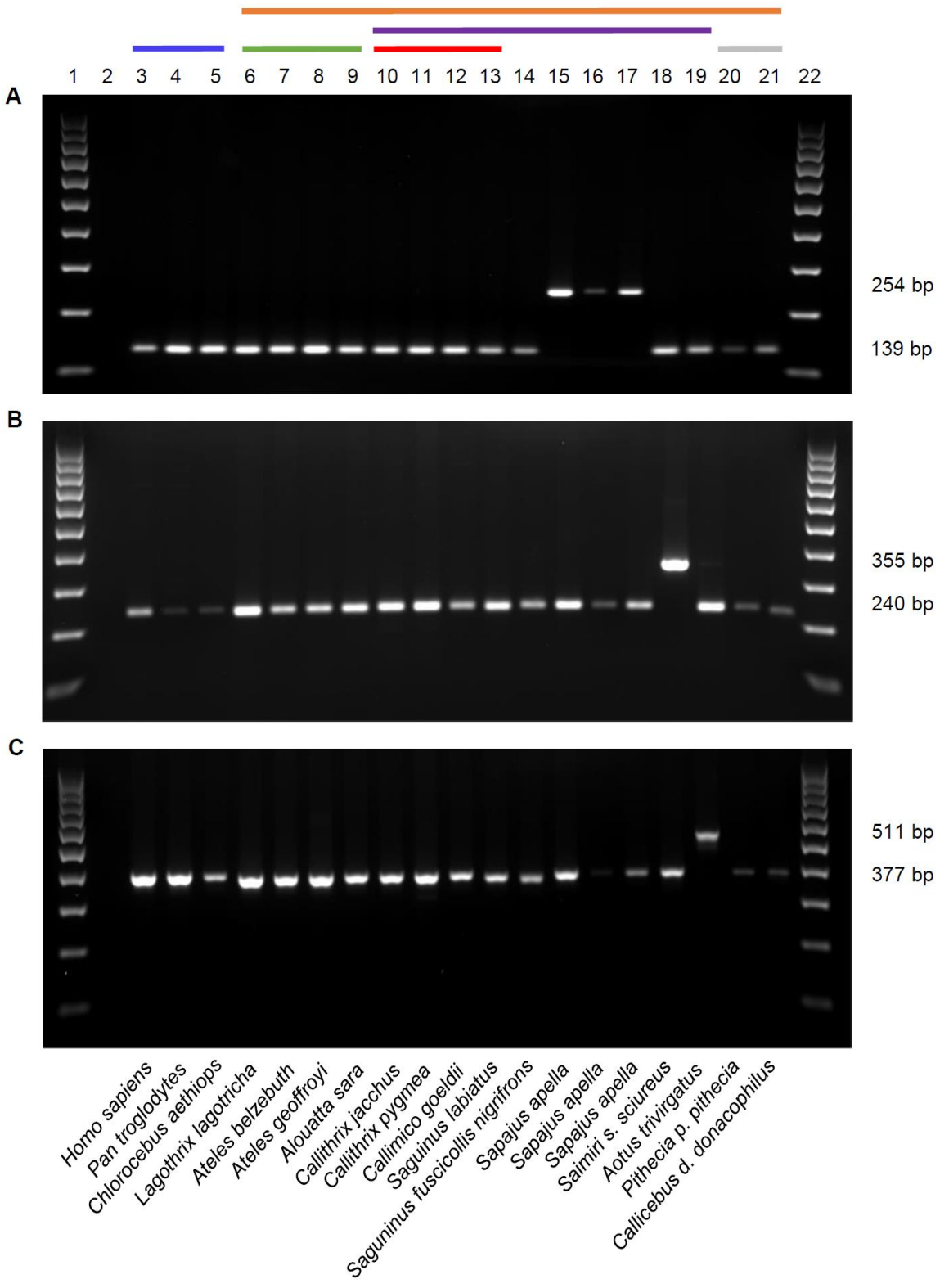
Lineage-specific Platy-1 insertions in NWM

A total of 387, 605 and 335 Platy-1 loci were retrieved from the RepeatMasker analysis of the capuchin [Cebus_imitator-1.0], owl monkey [Anan_1.0], and squirrel monkey [saiBol1] genomes, respectively (Table 2.2). Of these, 171, 378, and 158 were determined to be full-length insertions, as previously defined (See Materials and Methods (Konkel et al. 2016). These values are strikingly low as compared to the 2268 full-length Platy-1 elements previously identified in marmoset [calJac3] (Konkel et al. 2016). In the capuchin genome, there were 22 predicted lineage-specific Platy-1 insertions, with 16 insertions conducive to locus-specific PCR (Table

2.2, Figure 2.2A, Figure 2.3A). The squirrel monkey genome had a similarly low number of lineage-specific insertions, 36, with 18 of these analyzed by PCR (Table 2.2, Figure 2.2B, Figure 2.3B). With 145 loci, the owl monkey genome had the largest number of lineage-specific insertions of the three NWM genomes investigated. Of these, 119 insertions were analyzed using locus-specific PCR (Table 2.2, Figure 2.2C, Figure 2.3C).

Table 2.2. Platy-1 element summary. The table shows the total Platy-1 elements extracted from the RepeatMasker output (Total), the full-length elements extracted from the RepeatMasker output (Full-length), the elements that were predicted to be lineage-specific, and full-length loci analyzed using locus specific PCR for each NWM

	Total	Full-length	Lineage-specific	PCR
Capuchin monkey	387	171	22	16
Squirrel monkey	335	158	36	18
Owl monkey	605	378	145	119



(Caption on following page)

Figure 2.2. Lineage-specific Platy-1 elements. A) The presence of the Ceb_5 capuchin monkey specific Platy-1 element is indicated by the higher of the two bands present (254 bp band), while the absence is indicated by the lower of the two bands present (139 bp band). B) The presence of the Ply4a-27 squirrel monkey specific Platy-1 element is indicated by the higher of the two bands present (355 bp band), while the absence is indicated by the lower of the two bands present (240 bp band). C) The presence of the U_OM_89423_v3 owl monkey specific Platy-1 element is indicated by the higher of the two bands present (301 bp band), while the absence is indicated by the lower of the two bands present (200 bp band). Lanes: 1-100 bp ladder; 2-TLE (negative control); 3-Human (HeLa); 4-Chimpanzee; 5-African green monkey; 6-Wooly monkey; 7-White-bellied spider monkey; 8-Black-handed spider monkey; 9-Bolivian red howler monkey; 10-Common marmoset; 11-Pygmy marmoset; 12-Goeldi's marmoset; 13-Red-chested mustached tamarin; 14-Geoffroys saddle-back tamarin; 15-17-Capuchin monkey; 18-Squirrel monkey; 19-Owl monkey; 20-Northern white-faced saki; 21-Bolivian gray titi; 22-100 bp ladder. The bars above the gel electrophoresis image indicate the following: Blue-Old World Monkey; Gold-NWM; Green-Atelidae; Purple-Cebidae; Red-Callithrichinae; Grey-Pitheciidae. Scientific names of the primates are indicated below the gel images.

Of the capuchin monkey lineage-specific Platy-1 insertions, the majority belonged to the 4a subfamily (Figure 2.3A). All of the 16 loci subjected to PCR (See Materials and Methods) were homozygous for the presence of the insertion (Table A2.9). A similar trend was observed for the squirrel monkey lineage-specific insertions, as all 18 PCR-analyzed loci in this lineage were fixed present and the majority of these insertions also belonged to the 4a subfamily (Table A2.10, Figure 2.3B). The owl monkey genome had a considerably higher number of lineage-specific insertions, with the majority of the elements being either 4 or 4a subfamily members (Table 2.2, Figure 2.3C). Of the 119 loci analyzed by PCR, 88 were homozygous present, while 31 remained polymorphic for insertion presence/absence among 23 *Aotus* individuals analyzed (Table A2.11, Figure 2.2C, Figure 2.4). The *Aotus* genus was the only one of four genera in this study to show evidence of ongoing Platy-1 mobilization. Given the rapid radiation of these four genera as discussed in a review article by Schneider and Sampaio (2015), our data suggests the emergence of the 4a Platy-1 subfamily approximately between 19 and 20 mya.

Among the 31 polymorphic loci identified in the owl monkey genome, the allele frequency variation across 23 *Aotus* individuals revealed a distinct separation between the two recognized groups of owl monkey, red- and grey-necked (Menezes et al. 2010), for at least three loci. For these loci there was a clear separation of species with (homozygous present) and without (homozygous absent) a Platy-1 insertion (Table A2.11**,** Figure 2.4), reflecting the red-

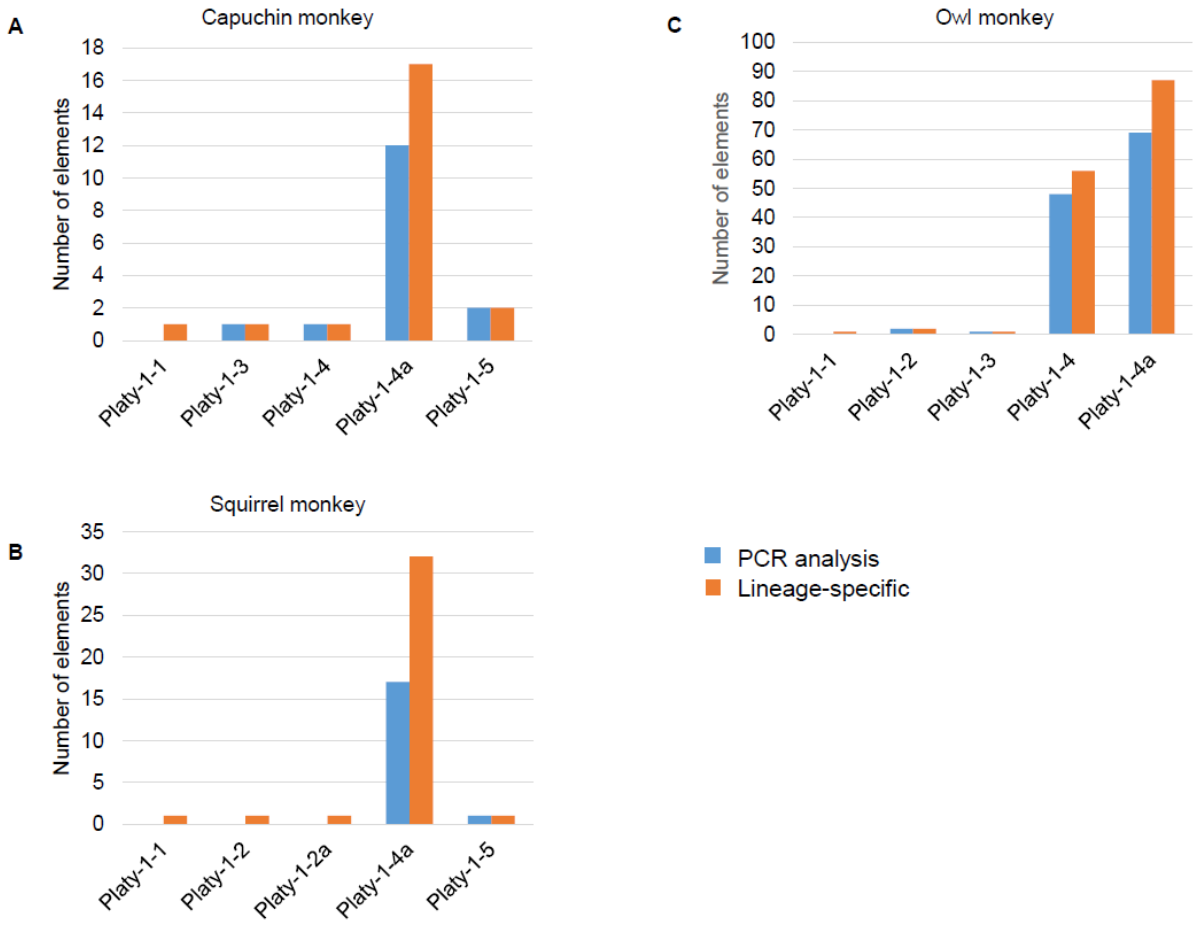


Figure 2.3. Predicted lineage-specific Platy-1 elements and PCR analyses. A comparison of the number of the predicted lineage-specific and PCR-analyzed loci is shown, as well as the number of elements belonging to each Platy-1 subfamily in the aforementioned categories. A) capuchin monkey B) squirrel monkey C) owl monkey. Note the differences in scale between capuchin and squirrel vs. owl monkeys.

necked (*A. nancymaae, A. azarae*) and grey-necked (*A. lemurinus, A. trivirgatus, A. vociferans*) divergence seen in South America (Menezes et al. 2010).

The majority of the lineage-specific Platy-1 elements discovered in this study were members of previously-defined Platy-1 subfamilies 4 or 4a based on the subfamily consensus sequences reported in Konkel et al. 2016. Evidence of recent mobilization within *Aotus,* and no observed mobilization activity among the *Saimiri, Cebus* or *Sapajus* genera prompted us to construct a sequence alignment of all owl monkey lineage-specific Platy-1 elements (Figure A2.1).

After comparing owl monkey-specific loci to the Platy-1-4 consensus sequence reported in Konkel et al. 2016, at least two distinct diagnostic mutations occurred since *Aotus* diverged from the other genera. Among the loci present in the owl monkey genome, there were multiple shared diagnostic mutations at positions 19 (G to C transversion), 26 (T to A transversion), 64 (G to T transversion), 70 (C to G transversion), 79 (C to T transition), and 82 (A to G transition). This newly discovered subfamily was named Platy-1-4b_*aotus* (n=58) and is aligned in (Figure 2.5). The nomenclature convention is as follows: this subfamily appears to have derived from Platy-1-4 but had different diagnostic substitutions than Platy-1-4a and was discovered in owl monkey.

Another diagnostic change was identified among *Aotus*-specific loci, some of which were fixed present while others were polymorphic. While sharing all diagnostic mutations that compose Platy-1-4b_*aotus*, there were three additional diagnostic mutations at positions 12 (G to A transition), 62 (A to G transition), and 100 (A to G transition). This new subfamily was termed Platy-1-4b3_*aotus* (n=10). This follows standard nomenclature for naming repeats, as this

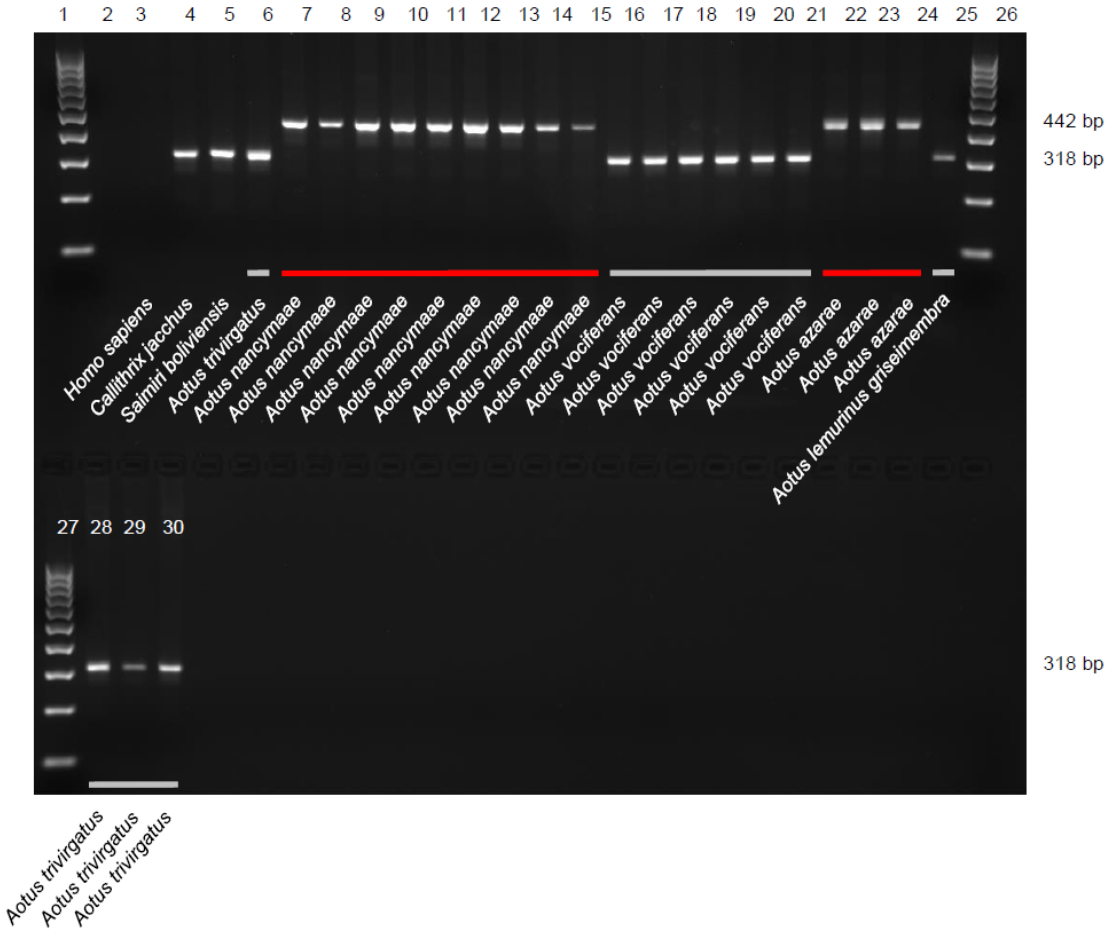


Figure 2.4. Polymorphic Platy-1 element in Owl monkeys. A gel image was generated subsequent to a PCR for site U_OM_87201 using primers that utilized the DNA from the owl monkey DNA panel. A band indicating a filled site is 442 bp while an empty site is indicated by a 318 bp band. Lanes: 1-100 bp ladder; 2-TLE (negative control); 3-Human (HeLa); 4-Common marmoset; 5-Bolivian squirrel monkey; 6-Three-striped owl monkey; 7-15: Nancy Ma's night monkey; 16-21: Noisy owl monkey (Spix's night monkey); 22-24: Azara's night monkey; 25-Panamanian night monkey; 26-27: 100 bp ladder; 28-30: Three-striped owl monkey. Scientific names of the primates are indicated below the gel images. The bars beneath the gel electrophoresis bands indicate the following: Red-red-necked owl monkeys; Grey-grey-necked owl monkeys. Note that all of the filled sites on the electrophoresis gel image belong to DNA samples corresponding to red-necked owl monkeys, while empty sites correspond to grey-necked owl monkeys.

subfamily has all the mutations of Platy-1-4b_*aotus* with 3 additional mutations ((Batzer et al. 1996); Figure 2.5). Platy-1 mobilization in the *Aotus* lineage is consistent with the stealth model

of SINE amplification dynamics (Han et al. 2005b) in which a few very old elements remain

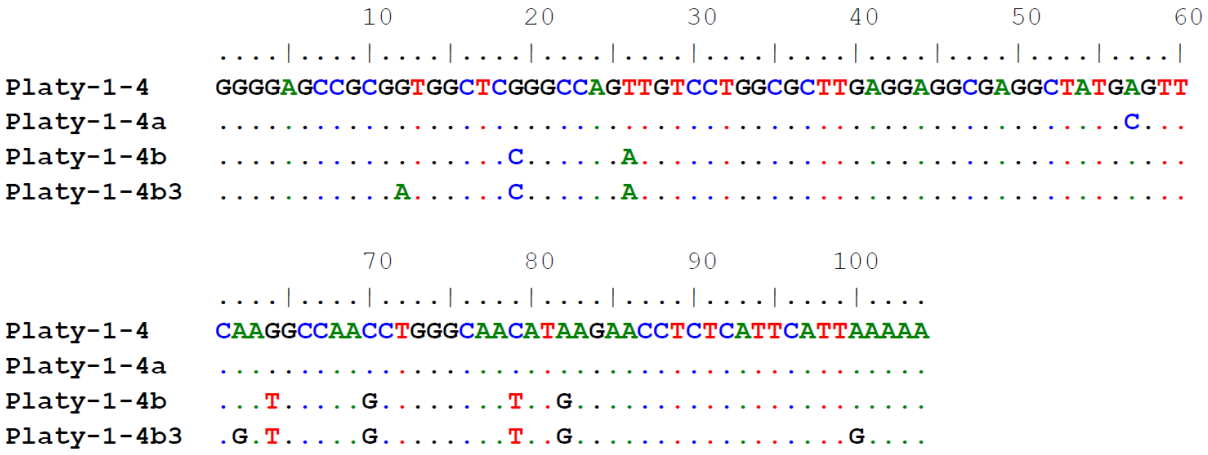


Figure 2.5. Platy-1 consensus sequence alignment. The consensus sequences of Platy-1-4 and Platy-1-4a were aligned to the newly discovered 4b_*aotus* and 4b3_*aotus* subfamilies discovered via an alignment of all of the full-length Platy-1 elements ascertained from the owl monkey genome. Dots represent a shared nucleotide while diagnostic substitutions are shown as the corrected base.

dormant for millions of years before slowly emerging with active daughter elements.

In the owl, squirrel and capuchin monkey genomes analyzed in this study, no Platy-1 subfamilies younger than Platy-1-1 to Platy-1-6 were identified in the initial RepeatMasker analysis. This is in contrast to the marmoset genome where 62 subfamilies were discovered and all are present in [calJac3] (Konkel et al. 2016). As a part of that initial marmoset study, a subset of Platy-1 elements representing the majority (50 of 62) of subfamilies were analyzed by PCR to assess their distribution among NWM species. A graphic illustration of those results is shown in: (Figure A2.2A). Subfamilies shared among all NWM on this graph belonged to the oldest subfamilies (Platy-1-1 through Platy-1-3) and one insertion specific to all Cebidae belonged to subfamily Platy-1-4a. These data are in agreement with the RepeatMasker analysis performed in

this study that identified the subfamily range between 4 and 4a as the source of lineage-specific elements reported here.

Divergence of Platy-1 subfamilies in NWM

Among the Platy-1 subfamilies there is a wide range of nucleotide divergence values from the respective subfamily consensus sequences as identified by RepeatMasker (Figure 2.6). A higher percent divergence from the respective subfamily consensus sequence is considered generally indicative of the age of the insertion event, as older elements have more time to accumulate random mutations. Mobile elements, on average, accumulate mutations at a neutral rate. As a consequence, the divergence can be used as an estimate of the age of the insertion. Figure 2.6 illustrates that the vast majority of the full-length Platy-1 elements identified in this study are relatively old. This finding is consistent with the PCR results from the squirrel and capuchin monkey lineage-specific DNA panels in which all the lineage-specific insertions had reached fixation throughout the genus. The average age corresponding with the percent divergence of the predicted lineage-specific Platy-1 insertions reported for the capuchin monkey is 12.4 mya with a range from 4.8 to 22 mya, while the average age of the lineage-specific Platy-1 insertions reported for squirrel monkey is 13.2 mya with a range from 3.2 to 27.7 mya. Older Platy-1 subfamilies correspond with higher percent divergence and therefore higher average age (e.g. capuchin monkey and squirrel monkey Platy-1-1: 21.8 and 23.4 mya, respectively) (Table A2.12, Table A2.13). This finding is in sharp contrast to the marmoset genome in which nearly 10% (224/2268) of the Platy-1 elements reported were nearly identical to their respective consensus sequences and almost 25% had a percent divergence of 1.5% or less (Konkel et al.

2016). However, the nucleotide divergences calculated for the older Platy-1 subfamilies discovered in the common marmoset genome are in agreement with the divergence estimates gleaned from the data in this study (Figure A2.2B).

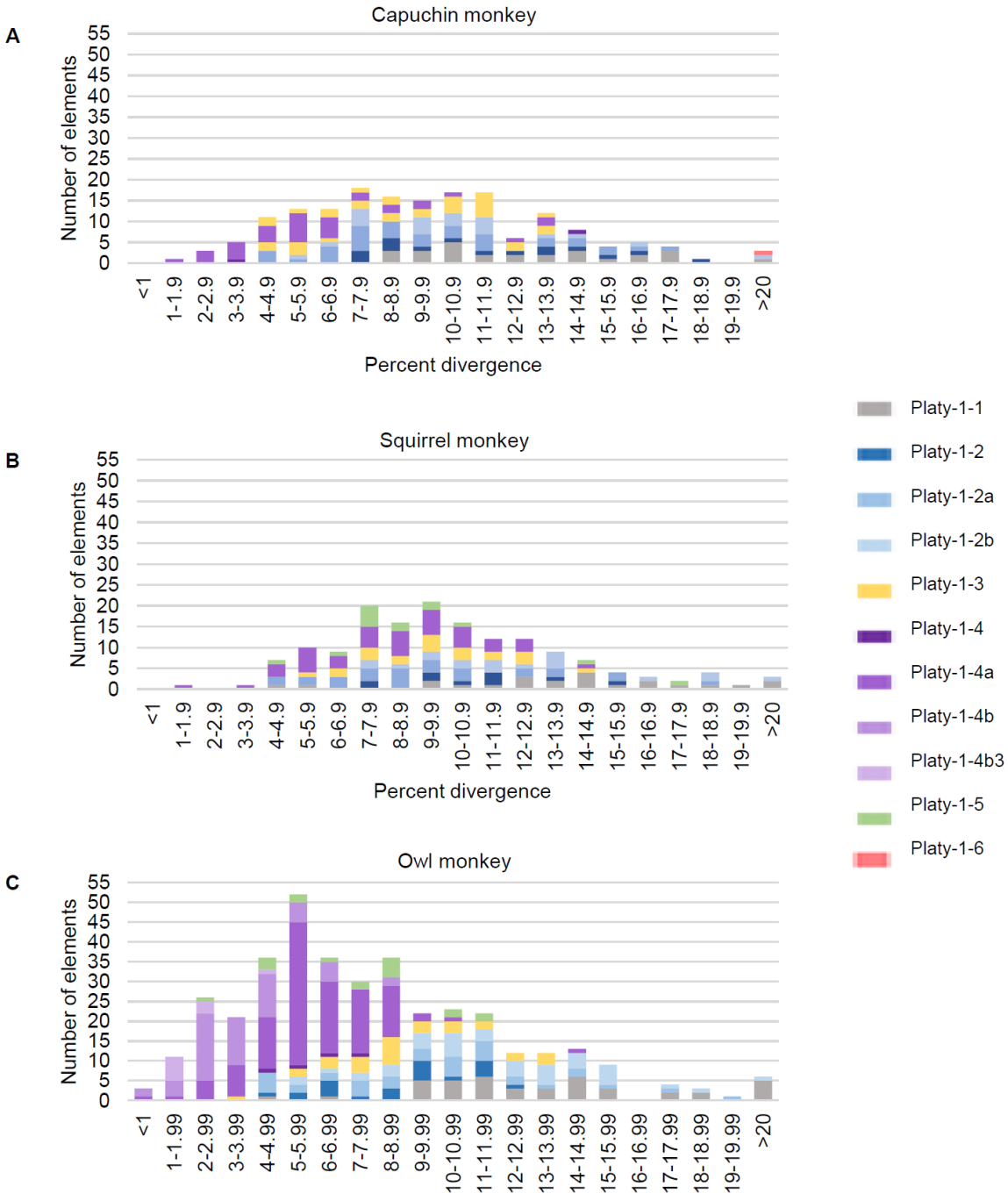


Figure 2.6. Platy-1 nucleotide divergence rates. Percent divergence from the subfamily consensus sequence of full-length Platy-1 elements. A) Capuchin monkey Platy-1 elements B) Squirrel monkey Platy-1 elements C) Owl monkey Platy-1 elements. The percent divergence was recorded from the RepeatMasker output.

The lower nucleotide divergence values of the Platy-1 insertions found in the owl monkey genome (Figure 2.6C) were consistent with more recent insertions and are in agreement with the polymorphic loci found via PCR. The average age of the predicted lineage-specific owl monkey Platy-1 insertions calculated from the percent divergence of the insertion sequence to its respective consensus sequence is 8.5 mya, with a range from 0 to 25.4 mya (Table A2.14).

It is of note that these age estimates are based on a retrotransposable element that is only ~100 bp in length and therefore could represent a fairly broad range. Even a one nucleotide change is equivalent to 1% divergence or about 1.66 million years. However, these results are intended to emphasize that the NWM genomes studied here contain primarily older Platy-1 elements, as compared to the marmoset genome in which the relative divergence values and age estimates illustrate that the marmoset genome contains large quantities of younger elements.

Shared Platy-1 elements

Over half (127/230; 55%) of the shared elements identified using a mugsy alignment (see Materials and Methods) were found within all four NWM genomes analyzed (marmoset, owl monkey, squirrel monkey, and capuchin monkey). The actual number is likely higher than this data set reflects due to lack of homology across multiple genome assemblies. These data are in agreement with the low number of lineage-specific insertions found in the NWM genomes analyzed in this study.

Five of the loci that were predicted to be lineage-specific in the squirrel monkey and capuchin monkey genomes were experimentally determined by PCR to be shared between the aforementioned genomes. These five loci were fixed present in all individuals representing the *Saimiri*, *Cebus* and *Sapajus* genera (Table A2.4). These data are consistent with the close established relationship between *Saimiri*, *Cebus* and *Sapajus*. In addition, these shared elements

all belonged to the 4a Platy-1 subfamily, indicating that the age of these elements could reflect the evolutionary divergence time of *Saimiri*, *Cebus* and *Sapajus* from other Cebids.

Discussion

This study expanded upon the research reported by Konkel et al. 2016 by not only recovering Platy-1 insertions unique to other NWM genomes, but also analyzing the amplification dynamics of these insertions. It is striking to note that there are a considerably lower number of Platy-1 repeats in owl, capuchin, and squirrel monkeys compared to the expansion and proliferation of Platy-1 insertions seen in the marmoset genome (Konkel et al. 2016). However, when comparing the three NWM genomes included in this study, there is a larger number of total, full-length, and linage-specific insertions found in the owl monkey genome than in the capuchin and squirrel monkey genomes (Table 2.2). Platy-1 mobilization in owl monkeys appears to have been relatively quiescent for millions of years, dating back to the 4a subfamily, and only recently resumed with modest retrotransposition activity leading to the origin of two new *Aotus* lineage-specific subfamilies. By contrast, Platy-1 retrotransposition in capuchin and squirrel monkeys remains quiescent. One possible explanation is polymorphic loci were subject to lineage sorting during speciation, potentially eliminating source drivers for Platy-1 mobilization. This explanation is consistent with the lower overall numbers of Platy-1 elements in the capuchin and squirrel monkey genomes and higher overall percent divergences of the elements from their consensus sequences. In addition, all of the lineage-specific loci ascertained from the capuchin and squirrel monkey genomes were determined to be fixed present. These data indicate negligible recent Platy-1 mobilization in these lineages. This slow propagation is likely not due to a lack of available enzymatic machinery as it has been shown that L1, the element that

provides the necessary enzymes for TPRT, has recently amplified in *Saimiri* among other NWM species (Feng et al. 1996; Boissinot et al. 2004).

These findings suggest that the extensive proliferation of Platy-1 elements in the common marmoset is the exception, rather than the norm in NWM genomes. Such disparities could be the result of differing effective population sizes after speciation, opposing environmental pressures, or genomic environment of the Platy-1 insertions in the different genera. There are also biological differences that might play a role. For example, marmosets have a unique aspect to their reproduction in that they mostly produce twins. The twinning of marmoset leads to genetic chimeras. This inherent genetic diversity in addition to the rapid reproduction of marmosets may have led to an environment favorable to retrotransposable element propagation. (Worley et al. 2014; Harris et al. 2014). The peak rate of Platy-1 propagation reportedly occurred with the rise of the marmoset ancestor (Konkel et al. 2016) when several Platy-1 subfamilies were active in parallel. In contrast, early Platy-1 evolution likely started with a low number of source elements resulting in very slow mobilization as illustrated by the NWM lineages analyzed in this study.

The polymorphic loci identified in this study that delineate between red-necked and grey-necked owl monkeys may be particularly useful for medical studies in which species identification is important. Owl monkeys have long been used as an animal model for malaria, with *Aotus lemurinus griseimembra* as the primary species used that is susceptible to the parasite responsible for causing this particular human malady (Herrera et al. 2002; Moreno-Perez et al. 2017). While other owl monkey species have varying degrees of malaria susceptibility, the results with *A. l. griseimembra* have been particularly reproducible. Another owl monkey species, *A. vociferans*, is also susceptible to infection, but not as widely used as *A. l. griseimembra.* It is of note that both of these species are considered grey-necked (Herrera et al.

2002). Having reproducible genetic markers to distinguish between grey-necked and red-necked owl monkeys may be of value for biomedical studies. Although only a few polymorphic loci were identified in the owl monkey genome, with a small fraction of those showing a clear separation between grey- and red-necked owl monkeys, these markers provide a quick, simple and unambiguous identification that is not currently available for this organism.

Platy-1 insertions observed in this study were often flanked by an *Alu* on either the 5' or 3' end of the Platy-1 element, and on rare occasions both sides. As reported by Konkel et al. 2016, Platy-1 elements with intact TSDs also possess endonuclease cleavage sites, indicating that Platy-1 elements have the same sequence and/or insertional preference as *Alu* elements.

Although Platy-1 elements may occasionally highjack *Alu* movement, Platy-1 elements are present in substantially lower overall numbers than *Alu* insertions in NWM. For example, a recent study of the *Saimiri* genome determined that there were 739,636 full-length and 43,201 lineage-specific *Alu* elements (Baker et al. 2017), a much higher number than the full-length and lineage-specific Platy-1 elements analyzed in this study. In addition, the majority of the Platy-1 elements characterized in this study were shared among all four of the NWM genomes studied. This indicates that there are simply not enough phylogenetically informative Platy-1 elements to be able to resolve NWM relationships. *Alu* elements may provide the key to elucidating NWM relationships as they have previously resolved difficult primate connections (Ray et al. 2005; McLain et al. 2012; Meyer et al. 2012; McLain et al. 2013; Walker et al. 2017; Jordan et al. 2018). A whole genome comparison of *Alu* insertion polymorphisms among the four NWM genomes described here may prove useful for elucidating some of the NWM relationships. A computational pipeline and a BLAT-based approach to identify shared *Alu* elements among NWM are explored in Chapters 3 and 4, respectively.

It is important to note that the repeats identified in this study were ascertained from the reference genome for all of the species studied. In addition, loci that were analyzed via PCR needed to be in conserved regions of all four genomes for confirmation of lineage-specificity. Sufficient time may have also passed that some of the insertions belonging to older subfamilies have experienced sufficient decay and were not recognized by RepeatMasker in the initial genome screening. It is therefore possible that the number of lineage-specific repeats and overall Platy-1 content in the NWM genomes analyzed is somewhat higher than reported. Undoubtedly, all three genomes have a sharply lower number of Platy-1 elements compared to marmoset.

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Chapter 3. Assessment of the polyDetect Computational Pipeline to Resolve the Cebidae NWM Phylogeny

Introduction

NWM, or Platyrrhines, is a parvorder of primates that all occupy the same general geography in South America (Perez et al. 2013). Although there are three NWM families, Cebidae, Atelidae and Pitheciidae, which are generally agreed upon, there is still conflicting information about the relationships within and between these three families (Schneider 2000; Schneider et al. 2001; Dyer et al. 2009; Menezes et al. 2010; Schneider and Sampaio 2015) potentially due to rapid speciation. Such rapid expansion is potentially rife with ILS.

Chapter 2 explored the amplification of a NWM specific retrotransposable element, Platy-1. However, due to the low number of Platy-1 elements in the owl monkey, capuchin monkey and squirrel monkey genomes, as well as the high percentage of Platy-1 insertions found at orthologous positions in all genomes, it was determined that Platy-1 elements would not be informative enough to resolve the position of the *Aotus* genus within the Cebidae lineage. Additionally, with so few insertions, the Platy-1 elements would not be able to overcome the potentially high levels of ILS in order to resolve this portion of the NWM phylogeny.

Recently, the controversial *Papio* baboon phylogeny was resolved using SRA (sequence read archive) data with the polyDetect program pipeline (Jordan et al. 2018). It was hypothesized that the same pipeline could be applied to *Alu* insertions from NWM SRA data to overcome previous difficulties that have arisen in attempts to resolve the Cebidae NWM phylogeny. The combination of the copy number and characteristics of *Alu* element insertions as well as the high throughput polyDetect program is a powerful method to analyze the position of the *Aotus* genus within Cebidae. Additionally, polyDetect makes use of a common reference sequence. The

subsequent output that uses the same coordinates for analyzing all SRA data is helpful in determining shared *Alu* insertions. This study attempts to elucidate one small portion of the NWM phylogeny; the position of the *Aotus* genus among the Cebidae family (Schneider 2000; Schneider et al. 2001; Schneider and Sampaio 2015) using the polyDetect pipeline and available SRA NWM data.

With the advent of faster and cheaper sequencing technologies comes a massive amount of data to sort through. Not only are model organisms sequenced but also non-model organisms allowing for a greater breadth and depth of research to be conducted. At its current pace the amount of genomic data doubles every seven months (Stephens et al. 2015). It is predicted that this will mean 2.5 million genomes sequenced by the year 2025 (Stephens et al. 2015), not including the number of individual human genomes that may be sequenced for personal or medical reasons. The question then is not about data availability, but how to accurately process and draw conclusions from the potentially heterogeneous data obtained from different tissues and species, as well as the type of sequencing performed, read depth coverage, assembly method etc., (Fan et al. 2014; Stephens et al. 2015). Keeping this potential data heterogeneity in mind, the pipeline was fully assessed for accuracy when applied in the current study. The application of the polyDetect pipeline to this portion of the NWM phylogeny highlights the limitations of this program when applied to highly diverged genera.

Materials and Methods

Alu Shared Elements

To analyze *Alu* elements found at orthologous loci in NWM (i.e., shared among NWM), the polyDetect pipeline was used as previously described (Jordan et al. 2018). Briefly, short read data (referred to as SRA data) from the common marmoset (*Callithrix jacchus*; caljac3),

capuchin monkey (*Cebus imitator*; Cebus_imitator-1.0), squirrel monkey (*Saimiri boliviensis*; saiBol1) and owl monkey (*Aotus nancymaae*; Anan_2.0) were downloaded from NCBI. Two sets of SRA data were utilized for each NWM. SRA data set 1 (DS1) included SRA files containing similar amounts of data to attempt to ensure even coverage for all organisms used (Coverage average ± standard deviation: 30.69 ± 2.96) with the same platform utilized for the common marmoset, squirrel monkey, capuchin monkey and owl monkey (Table A3.1). SRA data set 2 (DS2) contained SRA data for the same NWM as DS1, but the sequencing platforms and coverage vary (Table A3.2; Average coverage ± standard deviation: 261.31 ± 196.43). The pipeline then maps these reads to a common reference *Alu* consensus sequence via BWA mem (Li and Durbin 2009). The various reference *Alu* sequences utilized in this study were: *Alu*S, *Alu*Ta7, *Alu*Ta10 and *Alu*Ta15 (Ray and Batzer 2005). The *AluS* consensus sequence was obtained from RepBase (Jurka et al. 2005) while the *Alu*T consensus sequences were obtained from Ray et al. (2005). The *Alu* portion of the split-read was then cleaved and the remaining sequence mapped to a reference genome assembly using bowtie2 (Langmead and Salzberg 2012). The different NWM reference genomes used to map the remaining portion of the reads were: two NWM belonging to the Cebidae family (the common marmoset and the squirrel monkey), a member of the Pitheciidae family of NWM (the white-faced saki -*Pithecia pithecia*; PitPit_v1_BIUU) and a member of the Atelidae family of NWM (the black-handed spider monkey *Ateles geoffroyi*; AteGeo_v1_BIUU). The genomes for the white-faced saki and black-handed spider monkey were also obtained from NCBI. It should be noted that there was no similar SRA data available for the white-faced saki or the black-handed spider monkey. The resulting polyDetect output indicates the chromosomal location where an *Alu* insertion is found. All organisms whose SRA indicated that an *Alu* insertion was in that organism were listed in the

Table 3.1. Possible polyDetect output categories. The first column shows all the possible polyDetect output combinations. C', 'M', 'O' and 'S' indicate that an *Alu* insertion is present in the capuchin monkey, marmoset, owl monkey, or squirrel monkey SRA data, respectively. An 'x' in a row indicates the organisms in a category that would share an *Alu* insertion, while the exclusion of an organism from a category is indicated by a gray box in that row.

	Capuchin monkey	Marmoset	Owl monkey	Squirrel monkey
CMOS	x	x	x	x
CMO	x	x	x	
COS	x		x	x
CMS	x	x		x
MOS		x	x	x
CM	x	x		
CO	x		x	
CS	x			x
MO		x	x	
MS		x		x
OS			x	x
C	x			
M		x		
O			x	
S				x

polyDetect output, allowing for the identification of shared *Alu* loci. All possible combinations of organsisms sharing an *Alu* insertions are listed in Table 3.1. The polyDetect genotypes were used to generate a nexus file for PAUP analysis.

Phylogenetic analysis

A heuristic search was performed using PAUP* 4.0b10 (Swofford 2011). Because it is assumed that the absence of an *Alu* insertion is the ancestral state of each locus, Dollo's law of irreversibility was used in this analysis. All loci were set to Dollo.up in the PAUP* analysis. From the computationally derived genotype data obtained from the polyDetect program using DS1, a nexus file was generated using a custom python script. The presence of an insertion was scored as "1" for a filled site and "0" for an empty site. Ten thousand bootstrap replicates were performed with the maximum tree space set to all possible trees.

Lineage-specific *Alu* elements

The capuchin monkey, owl monkey, human (*Homo sapiens*; GRCh38.p13), common marmoset and squirrel monkey genomes were obtained from NCBI. The capuchin monkey and owl monkey genomes were analyzed for full-length *Alu* elements using RepeatMasker (RepeatMasker-Open-4.0). Full-length *Alu* elements are defined as possessing a start position no less than 4 bp and an end position not shorter than 267 bp. Full-length elements were extracted from the RepeatMasker output using a custom python script. These elements, along with 600 bp 5' and 3' flanking sequence, were then compared to the remaining genomes in a sequential BLAT (Kent 2002) in the following order: 1) human; 2) common marmoset; 3) capuchin monkey or owl monkey; and 4) squirrel monkey. A sequential BLAT included determining lineage specificity after each BLAT to a genome by using a custom python script that analyzes the BLAT output for gaps of a specific length when comparing the query and target sequences that would indicate an *Alu* element is present in the genome of interest, but not the target genome. Such lineage-specific *Alu* elements would then be assessed for lineage specificity in the next comparison genome. This process was completed until all aforementioned genomes were compared to the *Alu* elements ascertained from either the capuchin monkey or owl monkey genome. For both the capuchin monkey and owl monkey lineage specific *Alu* insertions, 100 randomly selected insertions were chosen for the design of oligonucleotide primers and PCR analysis.

Oligonucleotide Primer Design

The loci determined to contain *Alu* elements unique in the owl monkey or capuchin monkey genome were put into individual files containing the orthologous sequences from marmoset, squirrel monkey, owl monkey and capuchin monkey genomes. These sequences were

aligned using CLUSTALW (Thompson et al. 1994) and/or MUSCLE (Edgar 2004). Forward and reverse oligonucleotide primers for PCR were designed using Primer3 (v.0.4.0) and checked in BioEdit to ensure minimal mismatches to allow for the amplification of a PCR product in all genomes specified. In silico PCR (Kent 2002) was used to confirm the oligonucleotide primers would amplify only one product in multiple species (Table A3.3, Table A3.4).

DNA Samples

DNA samples are described in Table A2.5, Table A2.6 and Table A2.8. Briefly, there were three panels utilized for this study: a NWM panel (Table A2.5), an owl monkey panel (Table A2.8), and a capuchin monkey panel (Table A2.6). The NWM panel contained three Old World monkeys (OWM) and sixteen NWM species representing the three NWM families. This DNA panel was used to screen elements for lineage-specificity. The owl monkey panel included DNA samples from 23 individuals of the genus *Aotus* representing five species, and the capuchin monkey panel included DNA from 14 different capuchin monkeys, 8 *Cebus apella*, now considered genus *Sapajus apella* (Alfaro et al. 2012), and 6 individuals from genus *Cebus* including the *Cebus imitator* sample used as the reference genome.

PCR Amplification

PCR amplification was performed in 25 µL reactions containing 25 µg of template DNA, 200 nM of each primer, 1.5 mM $MgCl_2$, 10x PCR buffer (1x: 50 mM KCl; 10 mM TrisHCl, pH 8.4), 0.2 mM dNTPs, and 1 unit of *Taq* DNA polymerase. The PCR reaction protocol is as follows: 94°C for 1 min, 32 cycles of denaturation at 94°C for 30 s, 30 s at the appropriate annealing temperature (typically 57ºC), extension at 72°C for 30 s, followed by a final 72°C extension step for 2 min. Gel electrophoresis was performed on a 2% agarose gel containing 0.2 µg/mL ethidium bromide for 60 min at 180 V. UV fluorescence was used to visualize the DNA

fragments using a BioRad ChemiDoc XRS imaging system (Hercules, CA). If PCR results were weak or unresolved, the PCR reaction was repeated using hot-start with the JumpStart *Taq* DNA polymerase kit (Sigma Aldrich). Genotypes were recorded in a Microsoft Excel worksheet as (0,0) homozygous absent, (1,1) homozygous present or (1,0) for heterozygous (Table A3.5, Table A3.6)

Results

Computational NWM phylogeny assessing shared *Alu* insertions

Using DS1 SRA data, seven different polyDetect program runs were completed (Table 3.2). Runs one through four were completed with different *Alu* consensus sequences but the same reference genome, the common marmoset, to determine if the *Alu* consensus

Table 3.2. Different polyDetect program runs using the DS1 data set.

polyDetct Run #	Alu consensus	Reference assembly
1	*Alu*S	Common marmoset
2	*Alu*Ta7	Common marmoset
3	*Alu*Ta10	Common marmoset
4	*Alu*Ta15	Common marmoset
5	*Alu*Ta15	White-faced saki
6	*Alu*Ta15	Squirrel monkey
7	*Alu*Ta15	Black-handed spider monkey

sequence used would influence the program output. *Alu*T subfamilies are specific to NWM, with *Alu*Ta7 and *Alu*Ta10 common to all NWM, and *Alu*Ta15 specific to Cebidae (Ray and Batzer 2005). The results of the analysis completed with runs one through four are in Figure 3.1. The results of the polyDetect output for these four program runs are strikingly similar (Figure 3.1). This result is surprising, as the different subfamilies arose during different time points in primate evolution.

No lineage-specific insertions were observed in the polyDetect output for any of the organisms used. This contrasts with the initial use of this program to investigate the *Papio* lineage, where many lineage-specific insertions were found for all individuals analyzed (Jordan et al. 2018). In addition, the smallest category within every run was that of *Alu* insertions shared among all four NWM individuals (Category CMOS, Table 3.1). This is in contrast with previous analyses using *Alu* elements as phylogenetic markers (Ray and Batzer 2005; Ray et al. 2005; Osterholz et al. 2009) as well as the results using a different retrotransposable element, Platy-1,

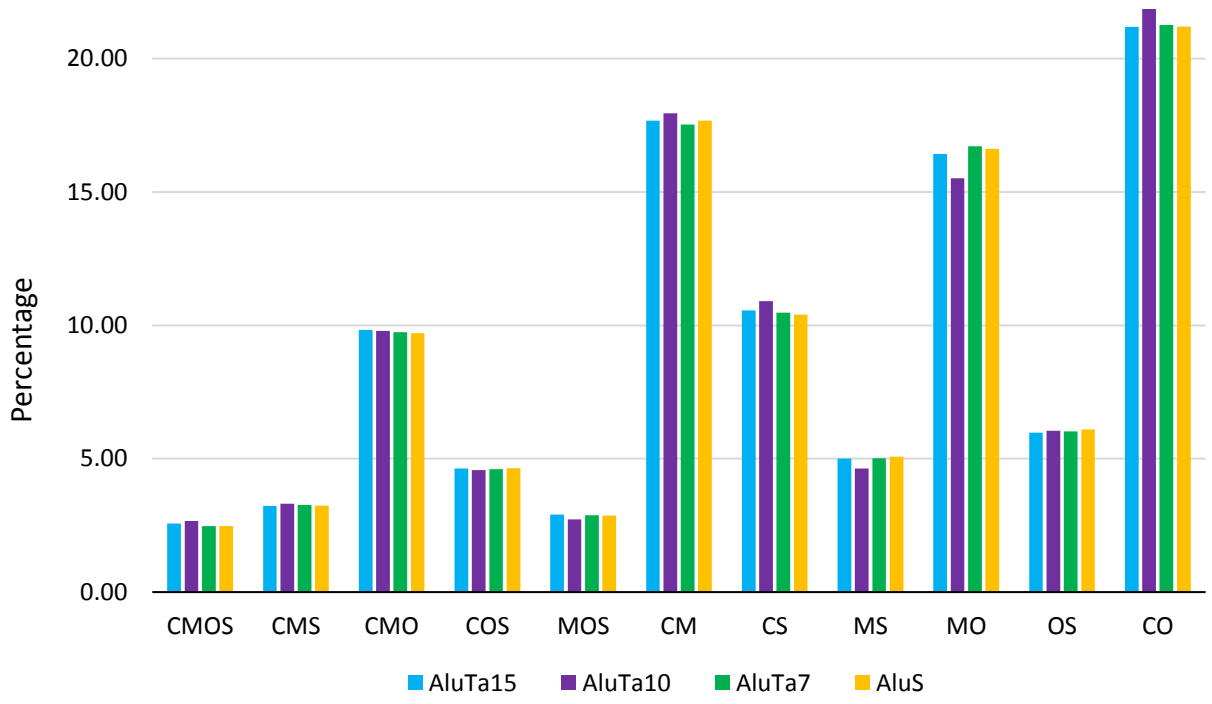

Figure 3.1. Output of the polyDetect program pipline using different *Alu* consensus sequences. The output of the polyDetect pipeline using the *Alu*Ta15 (blue), *Alu*Ta10 (purple), *Alu*Ta7 (green) and *Alu*S (yellow) consensus sequences. Each of these consensus sequences is associated with a different run of the program with the same DS1 data set is shown of the polyDetect program with the common marmoset as the reference genome assembly. The X-axis indicates pre-defined shared categories (Table 3.1). . Percentage on the Y-axis indicates the percent of the total number of predicted shared insertions as seen in polyDetect program output that belong to that category.

in which most of the elements found were shared by all NWM individuals analyzed (Storer et al. 2019).

The underlying principle of the polyDetect pipeline is homology of the SRA data to a selected reference genome and the *Alu* element consensus sequence. To test the hypothesis of low homology to the marmoset genome, three additional polyDetect program runs using DS1 with the *Alu*Ta15 as the reference *Alu* consensus sequence and three different reference NWM

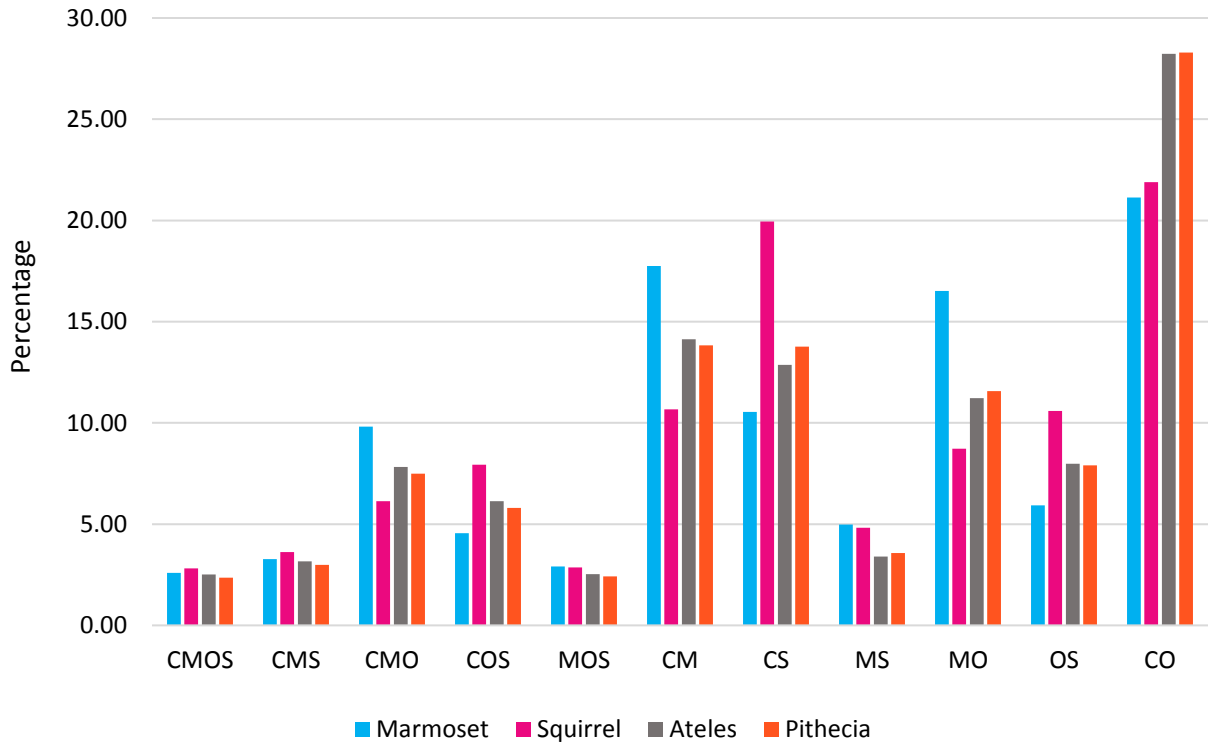

Figure 3.2. Output of the polyDetect program pipeline using different reference genome assemblies. The output of the polyDetect program using the common marmoset (blue), squirrel monkey (pink), black-handed spider monkey (grey) and the white-faced saki (orange) as the reference genome assembly. Each different genome assembly was a separate run on the polyDetect program pipeline. Each program was completed using the *Alu*Ta15 consensus sequence and the DS1 data set. The X-axis indicates pre-defined shared categories (Table 3.1). . Percentage on the Y-axis indicates the percent of the total number of predicted shared insertions as seen in polyDetect program output that belong to that category.

genome assemblies were completed (Figure 3.2). A similarly low percentage value of the total polyDetect output was observed in the CMOS with all the different reference genomes utilized. It was also noted that similar trends were observed for the two non-Cebidae reference genomes (Ateles & Pithecia), while the values for certain categories changed depending upon the Cebidae reference genome used. For example, the insertion percentage in the CM category (insertions shared between capuchin monkey and the common marmoset to the exclusion of owl monkey and squirrel monkey) was much higher when the common marmoset was used as the reference genome assembly than when the squirrel monkey was used as the reference assembly (18% and 11%, respectively). A trend was observed where if there was a category in which the reference genome was also a member, then there was an increase in that category relative to the other Cebidae reference genome and a corresponding decrease in categories where the reference genome was not a member, highlighting the influence of the chosen reference genomes on the polyDetect output. The categories CMO, CM, CS, MS, MO and OS were particularly sensitive to the phenomenon (Figure 3.2). However, overall similar trends were observed using different reference genomes with an emphasis on the low percentage of insertions shared by all NWM in this study and the absence of lineage-specific insertions identified.

An additional possibility is that DS1 did not contain adequate coverage of the different individuals. Therefore, a second data set, DS2, with larger SRA files and correspondning higher coverage was utilized. This data set used the *Alu*Ta15 consensus sequence and the marmoset genome as the reference genome assembly. It was observed that there was a percentage increase in the categories where squirrel monkey was a member (Figure 3.3). The percent increase indicates that the DS1 data set had lower sequence coverage of squirrel monkey compared to the other individuals in the same data set. The lower number of squirrel monkey calls was verified

by parsing through the polyDetect output (data not shown). Two categories showed a drastic change between data sets: CM and OS. From the smaller data set (DS1) to the larger data set (DS2) a large portion of the insertions belonging to the CM category were lost while insertions in the OS category were gained. It is possible that due to the increased overall sequence coverage in D S2 and increased coverage in the squirrel monkey individual in particular that there was a shift in the categories away from only being shared between capuchin monkey and marmoset to more genera. Therefore, higher coverage should lead to a large increase in the CMOS and CMS

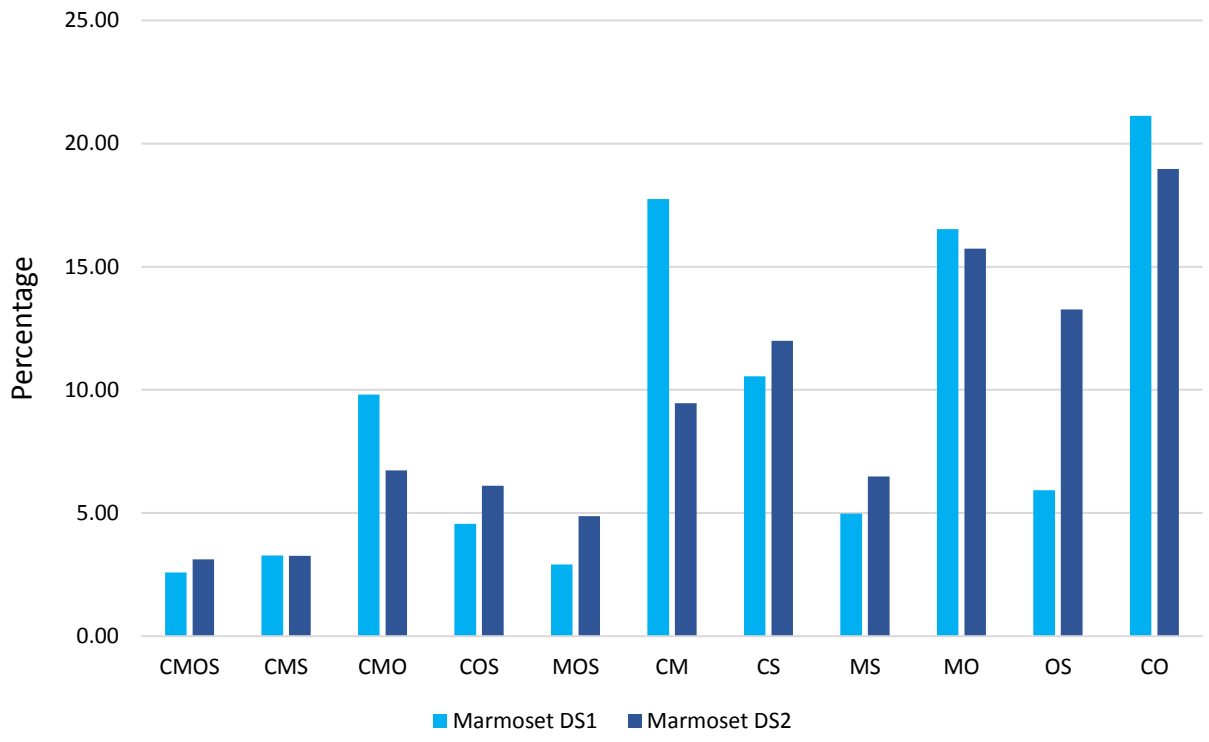

Figure 3.3. Output of the polyDetect program pipeline comparing two different SRA datasets. The polyDetect output is the result of using DS1 (light blue) and DS2 (dark blue). Both data sets were completed using the common marmoset as the reference genome assembly and *Alu*Ta15 as the *Alu* consensus sequence. The X-axis indicates pre-defined shared categories (Table 3.1). Percentage on the Y-axis indicates the percent of the total number of predicted shared insertions as seen in polyDetect program output that belong to that category.

categories. However, only a slight increase is observed between data sets in the CMOS category, with no change seen in the CMS category. Another possibility could therefore that the second data set has its own inherent level of coverage challenges with variable read quality for each individual.

PAUP analysis

The resulting phylogenetic trees produced by the pipeline output varied greatly depending on the different reference genomes utilized. The different topologies from the PAUP analysis using the different reference genomes show many possible phylogenetic scenerios (Figure 3.4). When the squirrel monkey genome was used as a reference there was a close relationship seen with the capuchin monkey genome with 99.36% bootstrap support for a branch that indicated squirrel and capuchin were sister to the exclusion of owl monkey and marmoset. In addition, there was 100% bootstrap support for a branch grouping capuchin monkey, squirrel monkey and owl monkey to the exclusion of marmoset. However, when either the white-faced saki or the black-handed spider monkey were used as the reference genome, there was 100% bootstrap support for capuchin monkey and owl monkey as sister groups with 100% bootstrap support for marmoset as the outgroup to capuchin monkey and owl monkey. When the marmoset genome was used as the reference genome, there was 84% bootstrap support for a branching pattern indicating marmoset and owl monkey as sister groups to the exclusion of the other two genomes. There was 100% bootstrap support for capuchin monkey as an outgroup to this branching pattern. In each of the trees generated (Figure 3.4), there were thousands of input loci

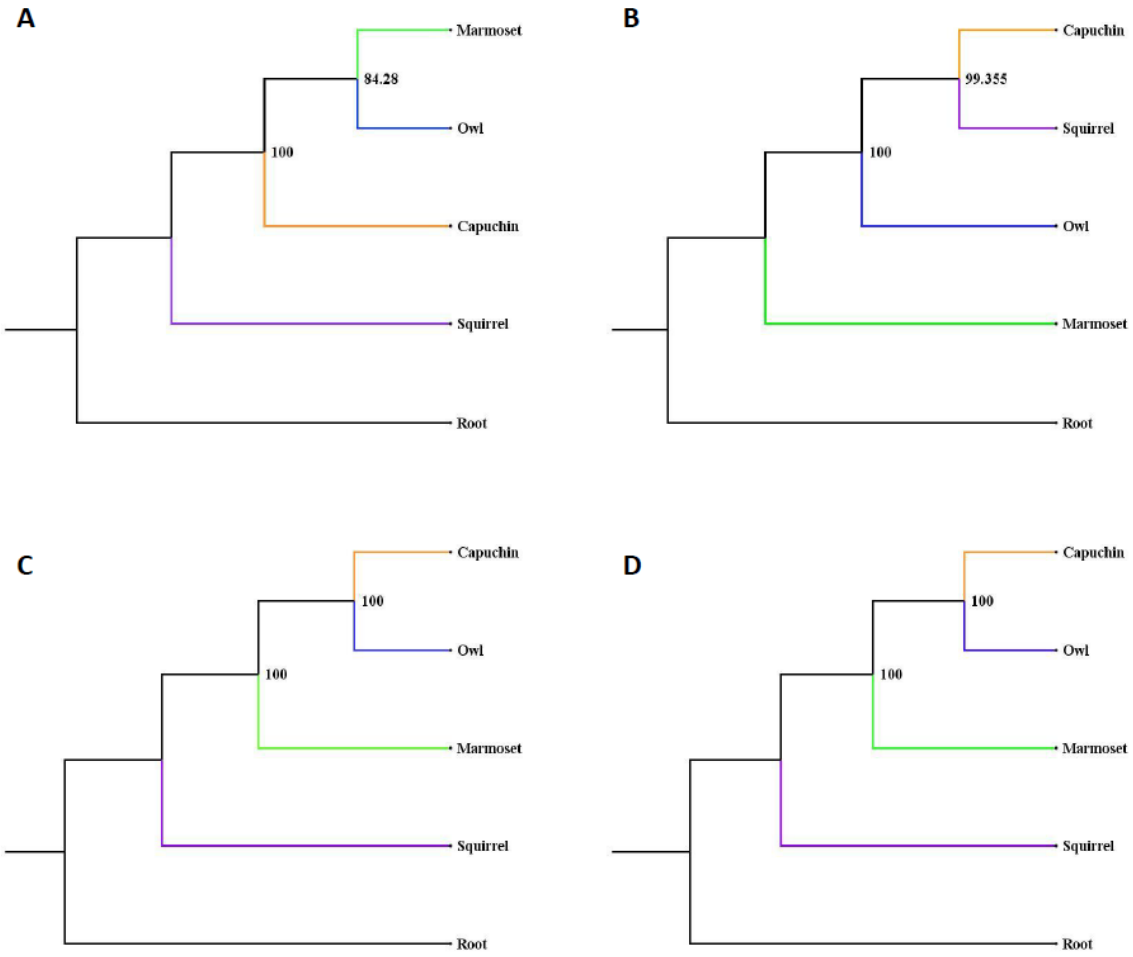

Figure 3.4. Phylogenetic analysis of the polyDetect pipeline output. A tree was generated using PAUP with the polyDetect data generated with the following reference genomes using DS1 with the *Alu*Ta15 consensus sequence: A) common marmoset B) squirrel monkey C) white-faced saki D) black-handed spider monkey. On each phylogeny the colors correspond to the following organism: green (marmoset), orange (capuchin monkey; referred to as, 'capuchin'), blue (owl monkey; referred to as, 'owl') and purple (squirrel monkey; referred to as, 'squirrel').

and thousands of phylogenetically-informative loci for any combination of reference genome and consensus *Alu* sequence analyzed (Table 3.3). However, the consistency index (CI), retention index (RI) and homoplasy index (HI) indicate that a significant amount of homoplasy is present

Table 3.3. PAUP input and parsimony statistics. C.I. (Consistency index); R.I. (Retention index); H.I. (Homoplasy index). Each row represents a separate polyDetect run with te reference genome and *Alu* sequence indicated.

DS1						
Reference genome	**Reference Alu**	**Characters**	**Phylogenetically informative**	**C.I.**	**R.I.**	**H.I.**
Ateles	AluTa15	7135	6955	0.549	0.531	0.451
Pithecia	AluTa15	7057	6890	0.545	0.527	0.455
Saimiri	AluTa15	8617	8374	0.541	0.512	0.459
Marmoset	AluTa15	8080	7871	0.549	0.529	0.451
Marmoset	AluSc7	8251	8046	0.548	0.528	0.452
Marmoset	AluTa7	8238	8033	0.549	0.53	0.451
Marmoset	AluTa10	8238	8033	0.549	0.53	0.451
DS2						
Marmoset	AluTa15	20871	20206	0.515	0.455	0.485

in each of the datasets. The high level of homoplasy could be the result of ILS. An HI closer to zero would indicate low homoplasy and a CI and RI closer to one would also indicate low homoplasy in the data set, whereas all indices are mid-range for every comparison reported here signaling potential inadequacies with this approach. It should be noted that there was no SRA data available for the white-faced saki or the black-handed spider monkey. However, use of their genome coordinates was used to generate nexus files for PAUP analysis and phylogenetic tree generation.

Interestingly, every tree generated from these comparisons showed that either marmoset or squirrel monkey was most basal while the capuchin monkey and owl monkey were never basal to all other NWM in this study. In addition, no differences in tree topology were observed with the use of lower (DS1) and higher (DS2) coverage data sets, although the branch indicating the capuchin monkey as the most basal of capuchin monkey, owl monkey and marmoset using the DS2 SRA data had lower bootstrap support (Figure 3.5).

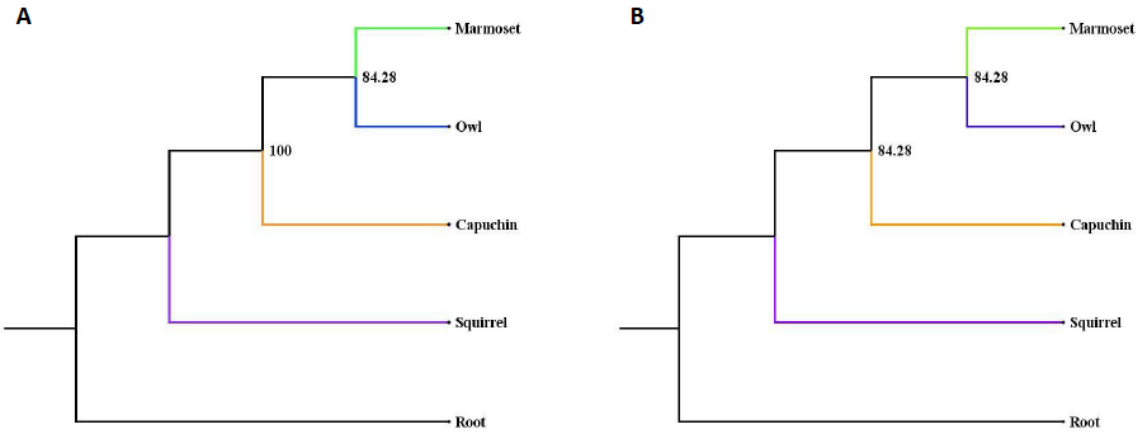

Figure 3.5. PAUP comparison between two SRA datasets. A tree was generated using PAUP with polyDetect data generated with the marmoset genome as the reference, the *Alu*Ta15 consensus sequence with the following SRA datasets: A) DS1 B) DS2. On each phylogeny the colors correspond to the following organism: green (marmoset), orange (capuchin monkey; referred to as, 'capuchin'), blue (owl monkey; referred to as, 'owl') and purple (squirrel monkey; referred to as, 'squirrel').

Lineage-specific insertions in the capuchin and owl monkey genomes

Previous studies have reported new *Alu* subfamilies and analyzed the number of lineage specific *Alu* element insertions in the common marmoset genome (Worley, et al. 2014) and the squirrel monkey genome (Baker, et al. 2017) but these analyses had not yet been conducted for capuchin or owl monkey. Due to the low number of insertions in the CMOS category in all analyses using polyDetect, it is possible that the number of lineage-specific insertions in two of the genomes not assessed for lineage-specific insertions, owl monkey and/or capuchin monkey, have a higher number of lineage-specific *Alu* elements, leading to a low number of shared elements by all four of the NWM tested here.

To test this hypothesis RepeatMasker analyses of the capuchin and owl monkey genomes were performed, providing 617,132 and 658,009 full-length *Alu* elements, respectively. Following the sequential BLAT (see Materials and Methods), 9602, or 1.55% of the 617,132 full-length *Alu* elements in the capuchin genome were lineage specific. The same procedure yielded 12,225, or 1.86% of the 658,009 full-length *Alu* elements that were lineage specific to the owl monkey genome.

To verify that this filtering procedure produced only lineage specific insertions, 100 randomly selected loci from each genome were analyzed via PCR on a NWM panel (Figure 3.6). Of the 100 random putative lineage specific *Alu* insertions ascertained from the capuchin monkey genome, 90 of these were determined to be specific to the capuchin monkey individuals on the DNA panel with 40 of these loci polymorphic for insertion presence / absence (Table A3.4). 4 of the 100 loci repeatedly failed to amplify a PCR product and were eliminated. Of the 100 random putative lineage specific *Alu* insertions recovered from the owl monkey genome, 88 of these loci were specific to owl monkey individualswith 19 of these loci being polymorphic for the insertion among *Aotus* samples (Table A3.6). 6 of the 100 loci from the owl monkey genome repeatedly failed to amplify during PCR and were discarded. These results verify that the method of filtering correctly identified lineage specific insertions.

Next, the full-length *Alu* insertions from both the capuchin and owl monkey genomes were compared against the human genome via BLAT to eliminate any *Alu* insertions that would be shared with primates before the rise of NWM. After this analysis, 58,952 and 77,564 insertions were remaining for the capuchin and owl monkey genomes, respectively. These numbers are far greater than the lineage specific insertions for each genome described above. Not including the linage specific insertions, there are 49,350 and 65,339 *Alu* insertions remaining

in the capuchin and owl monkey genomes, respectively. This indicates that the lineage-specific *Alu* insertions belonging to both of these genomes compromises a small portion of insertions compared to those that may be shared with other NWM. Therefore, the low number of insertions found in the CMOS category after completing the polyDetect pipeline is not due to a high number of lineage specific insertions in these two genomes, but rather due to lack of sufficient detection.

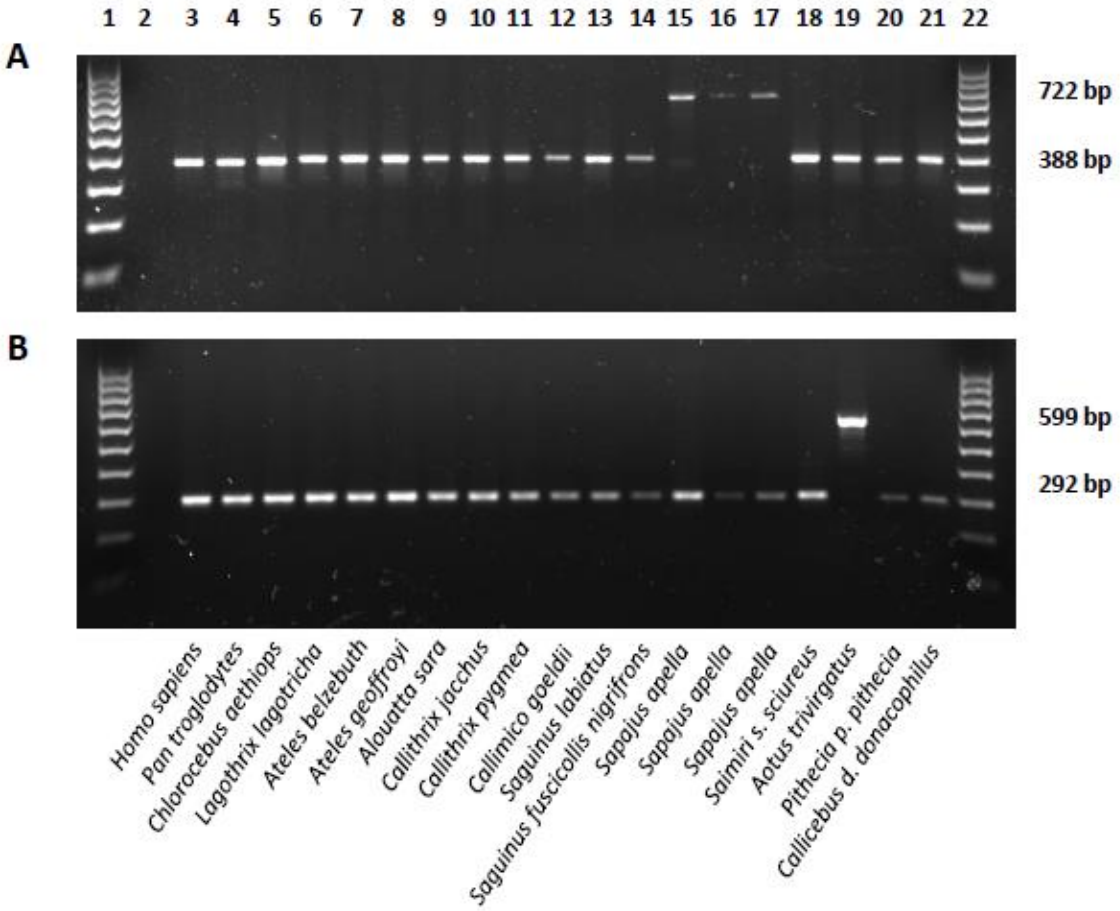

Figure 3.6. Lineage-specific *Alu* elements. A) The presence of the Cebus_738_016107358_8091150 capuchin monkey specific *Alu* element is indicated by the higher of the two bands present (722 bp band), while the absence is indicated by the lower of the two bands present (388 bp band). B) The presence of the Aotus_3842_018509268_1336944 owl monkey specific *Alu* element is indicated by the higher of the two bands present (599 bp band), while the absence is indicated by the lower of the two bands present (292 bp band). Lanes: 1-100 bp ladder; 2-TLE (negative control); 3-Human (HeLa); 4-Chimpanzee; 5-African green monkey; 6-Wooly monkey; 7-White-bellied spider monkey; 8-Black-handed spider monkey; 9-Bolivian red howler monkey; 10-Common marmoset; 11-Pygmy marmoset; 12-Goeldi's marmoset; 13-Red-chested mustached tamarin; 14-Geoffroys saddle-back tamarin; 15-17-Capuchin monkey; 18-Squirrel monkey; 19-Owl monkey; 20-Northern white-faced saki; 21-Bolivian gray titi; 22-100 bp ladder. Scientific names of the primates are indicated below the gel images.

Alignment of polyDetect predicted shared *Alu* elements

The primary benefit of having genome assemblies available for the NWM in this computational study is the ability to compare the polyDetect pipeline output data to the assembled genome sequences. To determine if the pipeline was predicting shared *Alu* elements correctly, the coordinates from ten randomly selected loci from each shared category from the polyDetect output were selected. 600 bp of flanking sequence were added to the 5' and 3' end of the predicted insertion point and the corresponding FASTA sequence extracted. The orthologous sequence from the capuchin monkey, owl monkey and squirrel monkey genomes were obtained via BLAT and aligned. All the predicted insertions were inaccurate and were in fact almost entirely shared by all four of the aforementioned NWM (Figure A3.1).

Filtering split-reads based on unique 5' flanking sequence

One possibility of inaccurate pipeline predictions could arise from the inaccurate map placement of an *Alu* element due to lack of sufficient unique 5' flanking sequence. A recent analysis using the polyDetect pipeline of *Alu* insertions shared between *Papio* baboons and a gelada monkeywas completed. Wet bench validation via PCR found that only 71% of the predicted calls by polyDetect were verified. After looking at the raw reads corresponding to a predicted *Alu* locus, it was found that longer flanking sequence corresponded with validated loci. The average TSD for retrotransposable elements that move via TPRT is 14 bp long (Konkel et al. 2015; Konkel et al. 2016). This is typically an A/T rich region. Therefore, the unique 5' flanking sequence past the *Alu* should reach past the TSD. Therefore, a 30 bp filter on split reads was imposed, where the minimum 5' flanking sequence in the read before the *Alu* insertion was 30 bp, which includes the 14 bp TSD and 16 bp additional flanking sequence. After this filter was imposed upon the read data obtained from DS2, the polyDetect program was completed using

the marmoset genome as a reference and *Alu*Ta15 as the *Alu* consensus sequence, and the output analyzed. After extracting the predicted insertion loci from the output of the program, the sequences were extracted in FASTA format from the marmoset genome as before and the orthologous sequence obtained via BLAT from the capuchin monkey, owl monkey and squirrel monkey genomes. Unfortunately, this additional filter, while helpful to other studies, such as the aforementioned baboon study, was not beneficial in this application. All of the loci analyzed were indeed inaccurate and were instead shared among all four NWM genomes (data not shown). This indicates that this pipeline is not a viable option for the reconstruction of the NWM phylogeny. It is possible that not enough homology exists for the short reads to map properly to the reference genome when multiple genera are being studied.

Alignment of SRA data to *Alu* consensus sequences

It is clear from the data presented thus far that the polyDetect pipeline is not applicable to this particular study. However, it is unknown at which point the error or problem occurs in the pipeline. There are two possibilities: either the SRA data is not aligning to the *Alu* sequence or after the alignment to the *Alu* consensus sequence there is not enough flanking to accurately map to the reference genome. Using the data from polyDetect run #4 (Table 3.2) as an example, the first alignment of the SRA data to the *Alu* consensus sequence using bwa mem was determined (Table 3.4).

Table 3.4: Output of bwa mem alignment of SRA reads to *Alu* consensus sequence for polyDetect run #4. PE (paired-end); SE (single-end). Both the common name for the organism and the organism ID from DS1 are used.

Organism	Percent PE reads aligned	Total PE reads	Percent SE reads aligned	Total SE reads
Squirrel monkey (84785)	49.69	2,281,688	44.19	14,709,295
Owl monkey (95829)	42.59	2,804,336	40.78	15,906,904
Capuchin monkey (35931)	65.21	1,803,178	55.72	9,083,234
Marmoset (35326)	92.77	401,458	91.29	5,060,388

These data indicate that alignment to the *Alu* consensus sequence was properly achieved as the percent of reads that aligned from the paired-end (PE) reads ranged from 42.59-92.77% and the single-end (SE) reads ranged from 40.78-91.29% (Table 3.4). This indicates that the bowtie2 alignment step of aligning *Alu* flanking sequence was inefficient, likely due to evolutionary decay of homologous sequence. In addition, the dataEval program, a part of the polyDetect pipeline, only analyzes split reads that match to the 5' end of the *Alu* consensus sequence. This could also result in a fewer number of shared *Alu* insertions. Therefore, the ~20 my divergence between the organisms used in this study could not be overcome with this pipeline.

Discussion

This analysis highlights the dangers of solely relying on computational data as well as the limitations of this computational pipeline. In the initial analysis using multiple different *Alu* consensus sequences it was clear that this pipeline may not be able to distinguish between different *Alu* subfamilies This is due in part to the age of each of the subfamilies with *Alu*S belonging to the oldest *Alu* family followed by *Alu*Ta7, then *Alu*Ta10, and ending with *Alu*Ta15 as the youngest subfamily. In addition, *Alu*Ta15 has been shown to be specific to the Cebidae

lineage (Ray and Batzer 2005). As such, it was hypothesized that most of the computationally derived insertions would belong to the *Alu*Ta15 subfamily. This potential disparity might have to do with the alignment of the reads to the *Alu* consensus sequence. The resulting position of the *Alu* insertion is based upon the 5' end of the *Alu* sequence. The 5' end of the *Alu* sequence contains the left monomer and the A and B boxes necessary for transcription by RNA polymerase III. Therefore, the 5' end of the *Alu* sequence would need to be highly conserved between subfamilies in order to preserve the A and B boxes, and consequently the first step in retrotransposon mobilization. The polyDetect pipeline alignment to the *Alu* consensus sequence may then not be sensitive enough to distinguish between *Alu* subfamilies.

In addition, when different reference genomes were used as a part of the polyDetect program, the output conflicted with previous studies. In particular, very few of the polyDetect run outputs displayed a high level of *Alu* insertions shared by all four NWM genomes studied. This is in contrast with previous studies that indicated that the majority of the *Alu* insertions were shared in all NWM genomes tested (Ray and Batzer 2005; Ray et al. 2005; Osterholz et al. 2009). In addition, there were no lineage-specific insertions found in any dataset. This is in contrast with the results ascertained from the marmoset (Worley et al. 2014; Konkel et al. 2016) and squirrel monkey (Baker et al. 2017) genomes that displayed large expansions of retrotransposable elements with an emphasis on *Alu* insertions. In addition, there are several thousand lineage-specific elements that were ascertained from the owl and capuchin monkey genomes as a part of this study, as well as polymorphic elements visualized via PCR.

The size and correlated coverage of the SRA data sets gave the same answer in terms of the phylogenetic output after PAUP analysis, although the data generated by using the larger SRA files (DS2) had poorer bootstrap support at one of the branch points. Even with higher

sequence coverage there were no lineage-specific elements and a low number of elements shared by all NWM found in this run using the DS2 dataset implying quantity does not always ensure quality.

When a phylogenetic analysis was completed using PAUP on the polyDetect output using the respective four NWM reference genomes, conflicting tree topologies were observed with high bootstrap support in each case. This indicates that the reference genome used greatly influences the output of this program most likely due to the homology-based nature of this program. Identical trees were observed when either the white-faced saki or the black-handed spider monkey genome was used. This is most likely a result of both of these NWM belonging to a family outside of the Cebidae lineage. Both NWM would therefore have the same relationship to the Cebidae lineage. It is also note-worthy that the RI, CI and HI of each tree was approximately equivalent and indicated a high amount of the phylogenetically informative loci used by PAUP contained a large degree of homoplasy.

When the sequences from the putative shared loci polyDetect output were extracted from the genome from which it was ascertained and an alignment performed with the orthologous sequence from the three remaining NWM genomes, it was discovered that almost all of those loci were actually shared among all four NWM genomes. This indicates that the exclusion of an organism from the polyDetect output does not necessarily indicate its absence. This information explains the high bootstrap support for conflicting trees, as the information used to generate those trees was not accurate. There are several possible explanations for inaccuracies in the polyDetect output. The first potential explanation is an issue with overall read coverage for repeat regions of the genome. It is possible that using the unassembled read data failed to identify unique *Alu* insertions with such short reads. The second potential source of error is

related to the comparisons being made. It is possible that the polyDetect program becomes less applicable as the species or genera of interest become farther diverged from one another.

The polyDetect pipeline was initially used for resolving the controversial baboon phylogeny resulting from a rapid divergence in the recent past and ongoing admixture within genus *Papio* (Jordan et al. 2018; Rogers et al. 2019). This study utilized the closely related rhesus macaque (*Macaca mulatta*) genome as the reference for the program producing highly reproducible and high confidence data that was verified comparing read data produced from 12 individuals representing 6 different species within the same genera. In contrast, the NWM used in this study belong to four different genera. In addition, the rapid 1-2 my divergence in the NWM lineage took place ~19-20 mya (Schneider 2000; Perelman et al. 2011). Because polyDetect is a homology-based program, this long time period of divergence might obscure any homology that could be detected in short read sequence data (Ewing 2015). In addition, there are two homology searches that occur sequentially. First, the reads are mapped to the *Alu* consensus sequence. The nucleotides in the short reads that mapped to the *Alu* were clipped and the second homology search to map the flanking sequence to the reference genome sequence was performed. As seen in Table 3.2, at least 40% of the reads effectively mapped to the *Alu*. It is also worth noting that of those reads that mapped to the *Alu* consensus sequence a portion of them mapped multiple times (data not shown). In addition, the highest number of elements in any data set in this study was 20,871 obtained from using the DS2 dataset, far below the expected number of *Alu* elements based on the literature. There are ~1 million *Alu* elements in primate genomes, with 600,000-730,000 of those elements constituting full-length repeats (Batzer and Deininger 2002; Deininger and Batzer 2002; Ray et al. 2005; Deininger 2011; Baker et al. 2017). Taken together, these results indicate that there was insufficient unique flanking

sequence to map to the reference genome to ensure accuracy in the program output for these highly divergent organisms.

These analyses indicate that the polyDetect pipeline is best suited to resolving phylogenies of closely related organisms, with an emphasis that those organisms belonging to the same genus, and when assembled genomes are not available for the organisms of interest.

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Chapter 4 Alignment and *Alu* Subfamily Analysis Approach to Resolve the Cebidae NWM Phylogeny

Introduction

In Chapter 3 the polyDetect program was applied to the Cebidae lineage of NWM phylogeny. However, the short reads did not allow for sufficient homology to accurately predict shared *Alu* insertions across NWM genera diverged by ~20 my (Schneider 2000; Perelman et al. 2011). The current study uses the genomes of those same four NWM used in Chapter 3 (marmoset, squirrel monkey, capuchin monkey and owl monkey), but uses the full *Alu* sequence extracted from the assembled genome with a combined total of 1200 bp of flanking sequence to provide adequate homology for a multiple sequence alignment. Previous analyses of the NWM phylogeny and *Alu* elements as a phylogenetic marker, although informative, were limited in their scope due to the lack of assembled genomes (Schneider 2000; Singer et al. 2003; Ray and Batzer 2005; Ray et al. 2005), whereas the sequence alignments constructed here provide a clear indication of which *Alu* insertions are shared among the NWM genomes analyzed and also reveal a high, and quantifiable, level of ILS across the four genera.

To complement this analysis, the evolution of *Alu* subfamilies in NWM was also explored. There are three main *Alu* families: J, S, and Y. *Alu*J can be found in all primates (Deininger and Daniels 1986; Deininger and Batzer 2002; Deininger 2011). *Alu*S arose from *Alu*J after the split between Strepsirrhines and what would become Platyrrhines and Catarrhines (Jurka and Smith 1988; Kapitonov and Jurka 1996). *Alu*Y is only present in Catarrhines (Batzer et al. 1991; Batzer et al. 1994; Konkel et al. 2010). Therefore, only *Alu*J and *Alu*S families are present in the Platyrrhine parvorder of primates. Lower case letters after the J, S or Y indicate a new subfamily derived from that *Alu* lineage. A Platyrrhine-specific *Alu* subfamily was

discovered that was a fusion event between Sc and Sp *Alu* elements, which was given a new name, T, following the standardized alphabetical nomenclature (Batzer et al. 1996; Ray and Batzer 2005). Numbers after lower case letters indicate that the subfamily is derived from the previously-defined subfamily, but differ by that number of nucleotides (Batzer et al. 1996).

Subfamily analysis of lineage-specific insertions can provide evidence of new *Alu* subfamily formation in many primate organisms. Some subfamilies can be shared by closely related taxa while others are unique to a given linage. This parallel evolution of *Alu* subfamilies leads to the formation of unique *Alu* subfamilies not shared with other lineages. Those combined subfamilies from closely-related taxa can then be used to generate a network and/or phylogenetic tree to determine which major *Alu* subfamily, or parental node, those younger subfamilies are derived from. In addition, this information may inform a phylogeny depending upon the *Alu* subfamily content and from which organism it was derived.

Previous analyses of lineage-specific subfamilies have provided potential biomedical and population genetics markers as well as highlighting the tempo of *Alu* amplification among various primates (Worley et al. 2014; Konkel et al. 2015; Baker et al. 2017; Steely et al. 2018). However, in the marmoset, squirrel monkey and baboon genome studies no standardized nomenclature was applied to the new *Alu* subfamilies discovered, although network analyses provide a general idea of where these elements fall in the *Alu*J, *Alu*S, *Alu*T or *Alu*Y subfamilies (Worley et al. 2014; Baker et al. 2017; Steely et al. 2018). A previous analysis of lemur *Alu* subfamilies identified new subfamilies derived from *Alu*J and named them *Alu*L in keeping with the nomenclature (Liu et al. 2009). The stepwise accumulation of diagnostic mutations can be used to generate a network of subfamilies and may inform any future *Alu* naming convention to accommodate the large number of new *Alu* subfamilies ascertained from the marmoset and

squirrel monkey genomes (Shedlock et al. 2004; Ray et al. 2007). Although a standardized nomenclature exists (Batzer et al. 1996), with the growing number of subfamilies the current framework is hard pressed to accommodate their rapid discovery in contrast to the historic pace of the discovery of *Alu* subfamilies (Batzer et al. 1995; Roy-Engel et al. 2001). For example, two new subfamilies were identified in the human genome related to the *Alu*Y subfamily. These two new subfamilies were termed *Alu*Yb8b1, *Alu*Yb7a3 and *Alu*Ya4a1, derived from *Alu*Yb8, *Alu*Yb7 and *Alu*Ya4, respectively (Konkel et al. 2015). Further expansion of subfamilies from these new lineages would lead to a very long and complicated names based on the current nomenclature.

This study combines all of the previous lineage-specific subfamilies discovered in the marmoset and squirrel monkey genomes and combines that information with lineage-specific insertions ascertained from the capuchin monkey and owl monkey as well as the subfamilies in RepBase (Jurka et al. 2005). The subfamily analysis provides insights into the evolution of the Platyrrhine parvorder by tracking which subfamilies were active in which genomes over time. In addition, this analysis provides a framework to revisit the *Alu* nomenclature to accommodate a larger number of *Alu* subfamilies.

Materials and Methods

Shared *Alu* elements

Each of four NWM genomes (common marmoset; caljac3, capuchin monkey; Cebus_imitator-1.0, squirrel monkey; saiBol1 and owl monkey; Anan_2.0) were obtained from NCBI and analyzed for their *Alu* content using RepeatMasker (RepeatMasker-Open-4.0). Full-length elements were parsed from the RepeatMasker output using a custom python script. Full-length elements, with 600 bp of 5’ and 3’ flanking sequence, for each genome were then

compared against the human genome using BLAT (Kent 2002). Lineage specificity compared to the human genome (*Homo sapiens*; GRCh38.p13) for each NWM genome was determined using a custom python script to determine if the appropriate *Alu* gap size was present between the query sequence and target human genome that would indicate the element was only in the query sequence. For each set of NWM *Alu* loci, the orthologous sequence was obtained from the three remaining NWM genomes via BLAT, aligned with MUSCLE (Edgar 2004) and placed into an alignment file. The average *Alu* insertion is ~300 bp, which includes the 3' A-rich tail. With the 1200 bp total flanking sequence, an ideal alignment would be a total of 1500 bp. In order to analyze the sequences and their alignments for *Alu* elements accurately, only alignments containing 1500-1600 bp were analyzed. Custom python scripts were used to analyze the alignment data. Briefly, each sequence from the four sequence alignment was scored based on

Table 4.1. Possible alignment output categories. The first column shows all the possible combinations. C', 'M', 'O' and 'S' indicate that an *Alu* insertion is present in the capuchin monkey, marmoset, owl monkey, or squirrel monkey genome, respectively. An 'x' in a row indicates the organisms in a category that would share an *Alu* insertion, while the exclusion of an organism from a category is indicated by a gray box in that row.

	Capuchin monkey	Marmoset	Owl monkey	Squirrel monkey
CMOS	x	x	x	x
CMO	x	x	x	
COS	x		x	x
CMS	x	x		x
MOS		x	x	x
CM	x	x		
CO	x		x	
CS	x			x
MO		x	x	
MS		x		x
OS			x	x
C	x			
M		x		
O			x	
S				x

the presence or absence of an *Alu* by aligning an *Alu*S consensus sequence to the aligned sequence from each of the four genomes and each alignment was parsed into a category based on the presence of an *Alu* in an orthologous position in another NWM genome (Table 4.1). The alignments were completed using the following parameters (using BioPython's PairwiseAligner): match_score=1.3; mismatch_score=0; target_open_gap_score=-1.0; target_extend_gap_score=-1.0; target_left_open_gap_score=-2; target_left_extend_gap_score= 0; target_right_open_gap_score= -1; target_right_extend_gap_score= 0; target_internal_open_gap_score=-5; target_internal_extend_gap_score=-3; query_open_gap_score= -5; query_extend_gap_score= -3; query_left_open_gap_score= -1; query_left_extend_gap_score= -1; query_right_open_gap_score= -2; query_right_extend_gap_score= 0; query_internal_open_gap_score=-5; query_internal_extend_gap_score=-3. A sample alignment is shown in Supplmental Figure A4.1. Randomly selected loci from each phylogenetically informative category (i.e., not lineage specific or shared between all four genomes) were analyzed via PCR (Table A4.1)

Oligonucleotide Primer Design

At least four randomly selected loci from each phylogenetically informative category were selected for oligonucleotide primer design. Forward and reverse oligonucleotide primers for PCR were designed using Primer3 (v.0.4.0) and checked with the alignment in BioEdit to ensure minimal mismatches to allow for the amplification of a PCR product in all genomes specified. In silico PCR was used to confirm the oligonucleotide primers would amplify only one product in multiple species.

DNA Samples

DNA samples are described in Table A2.5. The NWM panel contained three OWM and sixteen NWM species representing the three NWM families. This DNA panel was used to screen elements for shared *Alu* insertions.

Polymerase Chain Reaction (PCR) Amplification

PCR amplification was performed in 25 µL reactions containing 25 µg of template DNA, 200 nM of each primer, 1.5 mM $MgCl_2$, 10x PCR buffer (1x: 50 mM KCl; 10 mM TrisHCl, pH 8.4), 0.2 mM dNTPs, and 1 unit of *Taq* DNA polymerase. The PCR reaction protocol is as follows: 94°C for 1 min, 32 cycles of denaturation at 94°C for 30 s, 30 s at the appropriate annealing temperature (typically 57ºC), extension at 72°C for 30 s, followed by a final 72°C extension step for 2 min. Gel electrophoresis was performed on a 2% agarose gel containing 0.2 µg/mL ethidium bromide for 60 min at 180 V. UV fluorescence was used to visualize the DNA fragments using a BioRad ChemiDoc XRS imaging system (Hercules, CA). If PCR results were weak or unresolved, the PCR reaction was repeated using hot-start with the JumpStart *Taq* DNA polymerase kit (Sigma Aldrich).

Subfamily analysis

COSEG was applied to the lineage specific owl monkey and capuchin monkey *Alu* insertions (See Materials and Methods in Chapter 3) to determine the subfamily composition. Briefly, *Alu* insertions determined to be lineage specific were aligned via Crossmatch (www.phrap.org/phredphrapconsed.html) with the default settings, then analyzed via COSEG (www.repeatmasker.org/COSEGDownload.html) to determine subfamily structure. The data set was aligned against the *Alu*S consensus sequence (Jurka and Zuckerkandl 1991). COSEG was then used to group *Alu* subfamilies. The middle A-rich region of the *Alu*S consensus sequence

was excluded from analysis when determining subfamilies, whereas tri and di segregating mutations were considered. A group of ten or more identical sequences was considered a separate *Alu* subfamily.

The evolution of the combined aforementioned subfamilies was determined in the following manner: 189 subfamilies were subject to a RepeatMasker analysis of the consensus sequences obtained from RepBase (Jurka et al. 2005) and Ray & Batzer 2005 to generally place the subfamilies into a defined category (Jurka et al. 2005; Ray and Batzer 2005). The *Alu* subfamilies were then aligned in BioEdit and a network analysis completed based on the accumulation of diagnostic mutations (Figure A4.2). A summary of the RepeatMasker output by category and reasons for eliminating duplicate subfamilies can be viewed in Table A4.3.

Model selection

The 189 *Alu* subfamilies previously described were analyzed with jModelTest-2.1.10 (Darriba et al. 2012) to determine the best nucleotide substitution model for this data set. The Akaike information criterion (AIC) and Bayesian information criterion (BIC) models were a gamma distribution. Both the AIC and BIC model selection was TrN+G (variable base frequencies, equal transversion rates, variable transition rates, and gamma distributed rate variation among sites). The TrN+G model is in agreement with a previous analysis of *Alu* subfamilies derived from the squirrel monkey genome (Baker et al. 2017).

Bayesian phylogenetic analysis

An alignment of the 189 subfamilies was generated using MUSCLE (Edgar 2004). BEAST (Bayesian Evolutionary Analysis Sampling Trees) (Drummond et al. 2012) was used for Bayesian analysis and informed by using the jModelTest-2.1.10 analysis. All default settings were used with the following exceptions: site heterogeneity=gamma, species tree prior=birth

death process, nucleotide model=TrN, and chain length=30 million

Results

Shared *Alu* elements

The input full-length *Alu* sequences from marmoset, owl monkey, squirrel monkey and capuchin monkey were 61,513, 77,564, 32,145, and 58,952, respectively. These elements were obtained by extracting full-length *Alu* elements from each of the four NWM genomes in this study and only keeping elements that were lineage-specific when compared to the human

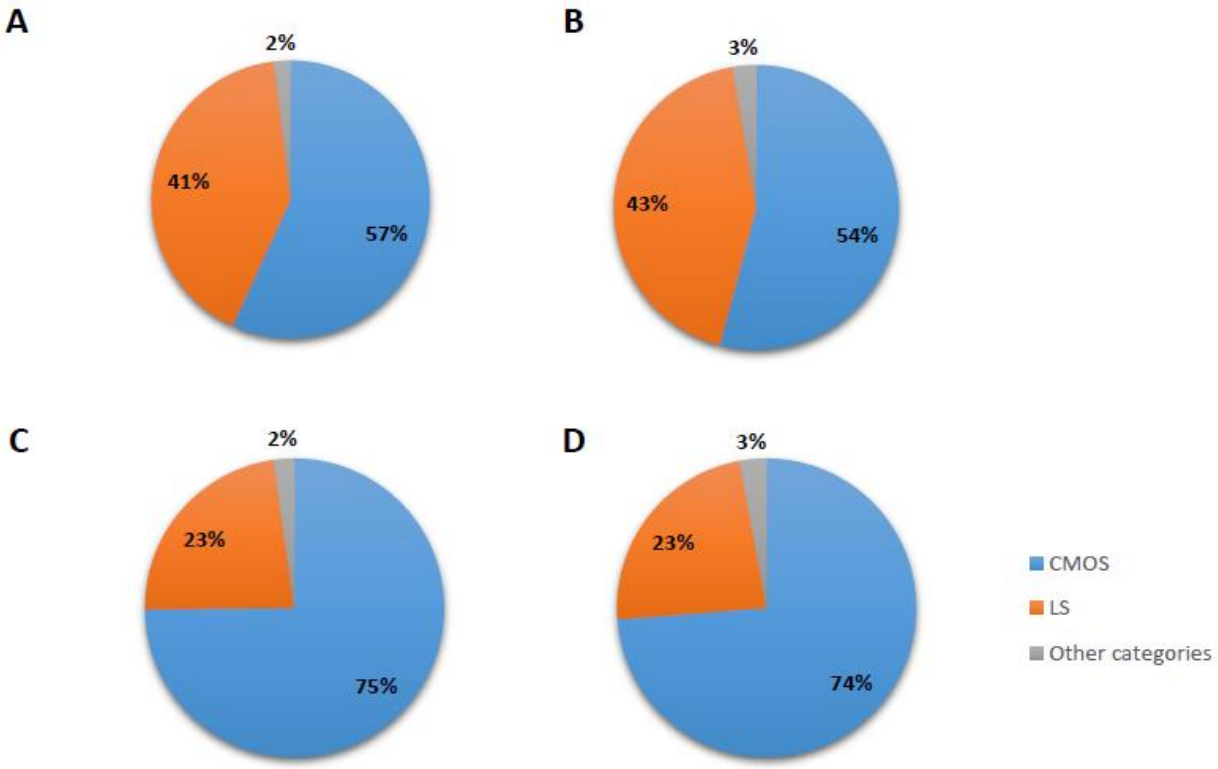


Figure 4.1. Distribution and genome comparison of shared and lineage-specific insertions. Alignments were categorized into pre-defined groups (See Materials and Methods) and then broadly characterized into three groups: LS (lineage-specific) in orange indicates the percent of the *Alu* insertions that were not found in orthologous position in any other genome. CMOS in blue indicates the percent of the elements from the BLAT analysis that were shared by all four NWM genomes. A) marmoset B) squirrel monkey C) owl monkey D) capuchin monkey.

genome. After orthologous sequence extraction and subsequent alignment, 51,320, 65,119, 28,614 and 49,093 aligned elements remained in the marmoset, owl monkey, squirrel monkey and capuchin monkey, respectively. After imposing the 1600 bp sequence limit upon the alignments, 35,680, 39,349, 19,919, and 31,479 alignments remained for elements obtained from the marmoset, owl monkey, squirrel monkey and capuchin monkey, respectively. The *Alu* elements extracted from each of the four NWM genomes and subsequent alignment analysis indicated that the majority of the elements were either shared among all four NWM tested or lineage-specific to the organism it was ascertained from (Figure 4.1). There were *Alu* insertions present in all phylogenetically-informative categories, although certain categories contained larger combined numbers than others (Figure 4.2). For example, when viewing the numbers of *Alu* elements shared between two organisms, CS (elements shared between capuchin monkey and squirrel monkey to the exclusion of marmoset and owl monkey) had a higher overall combined number. When considering those categories of *Alu* elements that were shared by three organisms to the exclusion of the other, COS was the group with the highest combined number

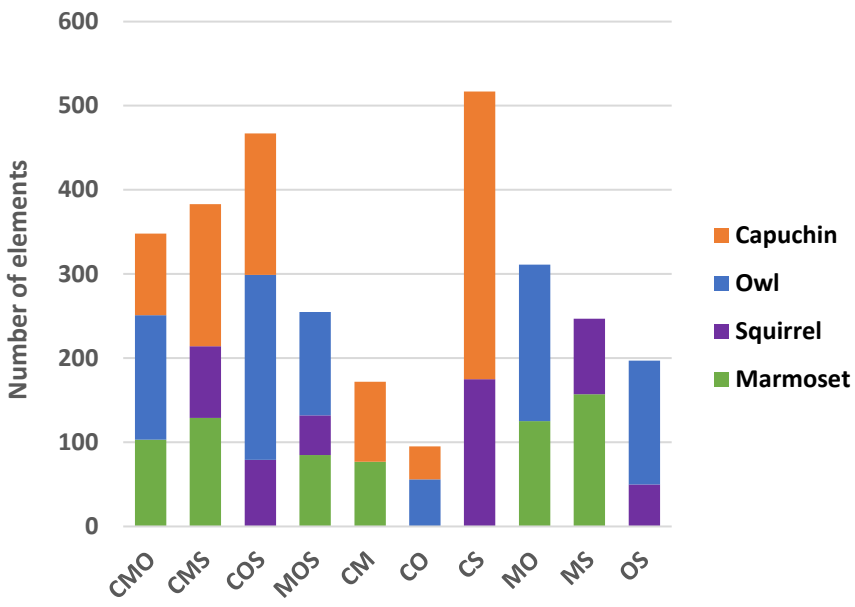


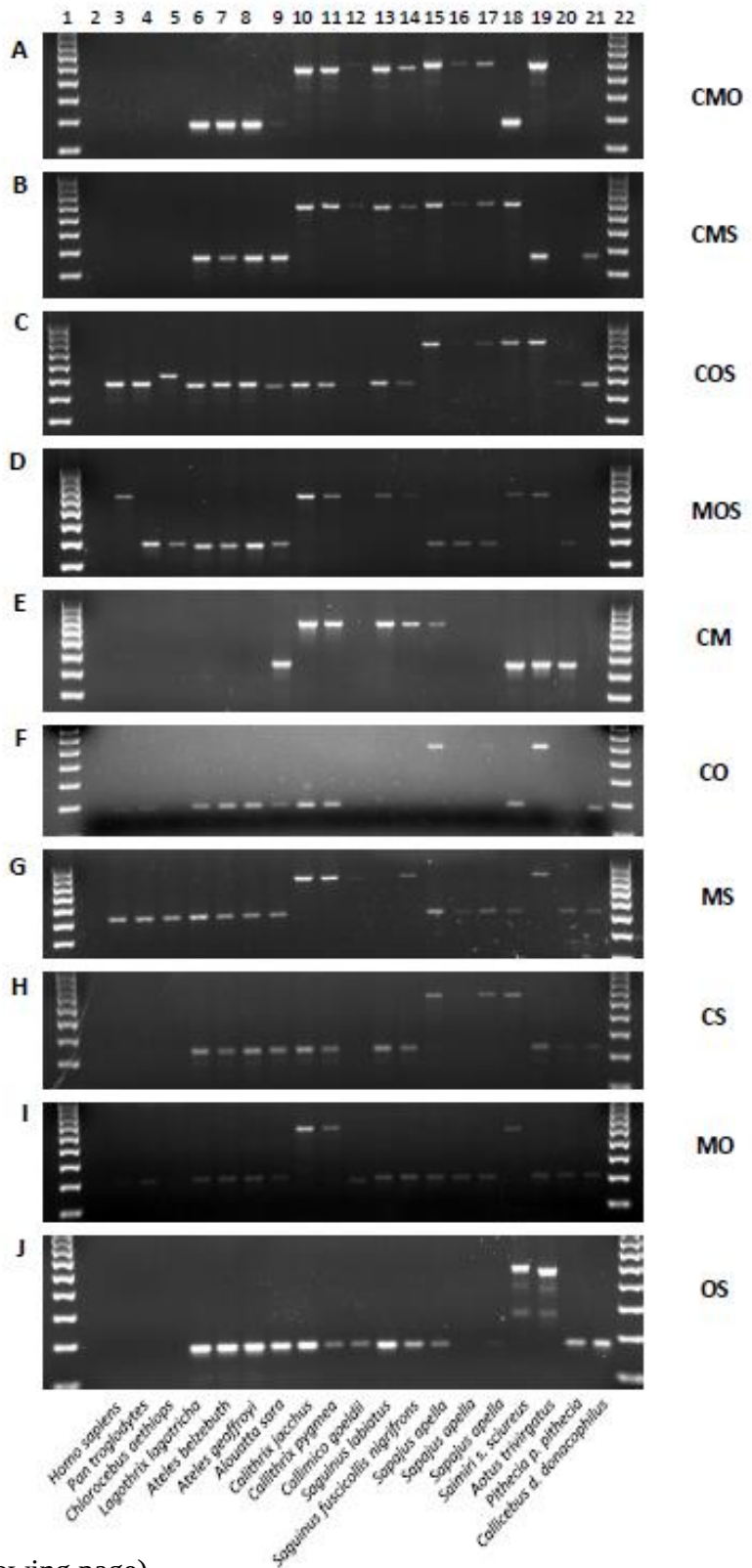
Figure 4.2. Comparison of phylogenetically-informative *Alu* alignments ascertained from the four NWM genomes. Orange, blue, purple and green indicate *Alu* elements ascertained from the capuchin monkey, owl monkey, squirrel monkey and marmoset genomes, respectively. Groups with shared elements on the x-axis refer to pre-defined groups (See Materials and Methods).

(Figure 4.2). Presence of *Alu* insertions in all phylogenetically-informative categories indicates that either ILS, near parallel or precise parallel insertions have occurred and are reflected in the data. This computational analysis was complemented by PCR. Randomly selected loci from phylogenetically informative loci analyzed via PCR confirms that there are shared *Alu* insertions representing each phylogenetically-informative group (See Materials and Methods; Figure 4.3). Taken together, these data confirm evidence of ILS.

Lineage specific *Alu* elements in the owl monkey and capuchin monkey genomes

An initial COSEG analysis of the lineage specific *Alu* elements in the capuchin genome indicated that there were 16 subfamilies present. However, upon closer analysis of the data, it was observed that some of the subfamilies had very long 3' A-tails which comprised half of the

consensus sequenced predicted by COSEG, or a long middle A-rich region. Upon inspection of the COSEG input capuchin monkey *Alu* insertions it was found that there were several hundred *Alu* sequences that contained a string of N's. These sequences were removed and the COSEG analysis was repeated. Nine and thirty subfamilies were obtained from the capuchin monkey and owl monkey COSEG analyses, respectively (Table A4.3, Figure A4.2).



(Caption on following page)

Figure 4.3. PCR analysis of phylogenetically informative *Alu* element categories. A) CMO_blat_2 B) CMS_blat_1 C) COS_blat_4 D) MOS_blat_2 E) CM_blat_2 F) CO_blat_4 G) MS_blat_4 H) CS_blat_2 I) MO _blat_2 J) OS_blat_4. Lanes: 1-100 bp ladder; 2-TLE (negative control); 3-Human (HeLa); 4-Chimpanzee; 5-African green monkey; 6-Wooly monkey; 7-White-bellied spider monkey; 8-Black-handed spider monkey; 9-Bolivian red howler monkey; 10-Common marmoset; 11-Pygmy marmoset; 12-Goeldi's marmoset; 13-Red-chested mustached tamarin; 14-Geoffroys saddle-back tamarin; 15-17-Capuchin monkey; 18-Squirrel monkey; 19-Owl monkey; 20-Northern white-faced saki; 21-Bolivian gray titi; 22-100 bp ladder. Scientific names of the primates are indicated below the gel images. Letters on the right side of the gel image coorespond with those found in Table 4.1

Alu subfamily network analysis

A total of 189 unique subfamilies were used to generate a network analysis based on the stepwise accumulation of diagnostic mutations. These subfamilies were derived from lineage-specific COSEG analyses of the marmoset, squirrel monkey, owl monkey and capuchin monkey genomes, and contributed 86, 46, 25 and 8 subfamilies, respectively. 5 owl monkey subfamilies of 30 defined in the COSEG analysis and 1 capuchin monkey subfamily of 9 subfamilies defined in the COSEG analysis were removed as these were exact matches to other previously-defined subfamilies (Table A4.3) 24 subfamilies had been previously defined in RepBase.These non-overlapping datasets show that capuchin monkey contributed very few lineage-specific subfamilies compared to the three other NWM in this study, indicating that there has been minimal expansion of *Alu* subfamilies in capuchin monkeys. The large expansion of *Alu* subfamilies in marmoset compared to the other NWM genomes is in agreement with the same differential expansion of Platy-1 elements (Konkel et al. 2016; Storer et al. 2019).

The RepeatMasker analysis of the 189 subfamilies used to identify which of four major *Alu* subfamilies (J, S, Ta10 and Ta15) the 189 subfamilies belonged to is available in Appendex

A (Table A4.2). The subfamilies that belonged to any *Alu*J subfamily (Jb, Jo, Jr and Jr4) were only observed from lineage-specific subfamilies ascertained from the marmoset genome (Figure 4.4; Table A4.2). Branches containing older *Alu*S subfamilies (Sp, Sq, Sq2, Sq10, Sx, Sx1, Sx3, Sx4, Sz, Sz6) also only contained subfamilies ascertained from lineage-specific marmoset subfamilies (Figure 4.4; Figure 4.5 Table A4.2). Branches with intermediate *Alu*S subfamilies (Sg, Sg4, Sg7) contained lineage-specific subfamilies from marmoset as well as squirrel monkey and owl monkey (Figure 4.4; Figure 4.5). The youngest *Alu*S subfamily branch, Sc, contained subfamily representatives from all lineage-specific sets (marmoset, squirrel monkey, capuchin monkey and owl monkey). The *Alu*Ta10 group was highly represented by lineage-specific squirrel monkey subfamilies, but was also found in lineage-specific insertions ascertained from all four genomes present (Figure 4.4; Figure 4.6). The *Alu*Ta15 group had high contributions from both the marmoset and squirrel monkey lineage-specific subfamilies, with lower numbers of lineage-specific owl monkey and capuchin monkey subfamilies (Figure 4.4; Figure 4.7).

The eight subfamilies contributing to this dataset from the capuchin monkey were only observed as being closed related to younger *Alu* subfamilies, suggestive of recent, but minimal, lineage-specific retrotransposition activity (Figure 4.4; Figure 4.5; Figure 4.6; Figure 4.7). Both squirrel monkey and owl monkey lineage-specific subfamilies contributed to the intermediate group of the *Alu*S subfamilies, while marmoset lineage-specific elements were found in the oldest *Alu*S subfamily groups as well as the oldest *Alu* subfamily groups belonging to *Alu*J (Figure 4.4; Figure 4.5). Within the *Alu*Ta15 subfamily branch the majority of the monophyletic groups belong to one taxa. (Figure 4.7). Note that the parentheses shown in Figure 4.5, Figure 4.6 and Figure 4.7 indicate the number of distinct diagnostic mutation differences from the parent node to the subfamily.

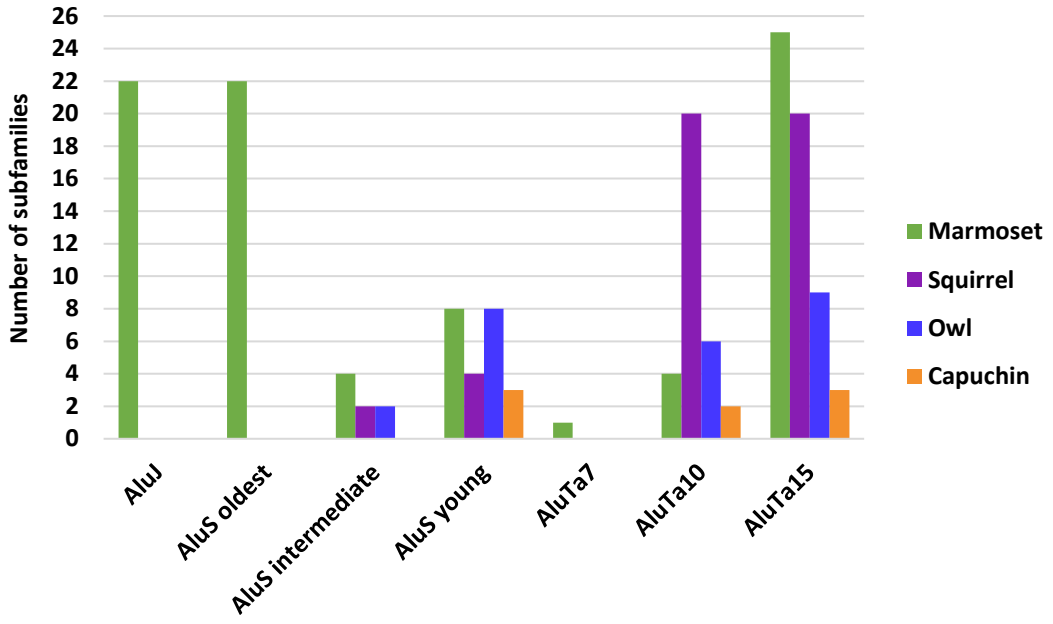


Figure 4.4. Lineage-specific subfamily RepeatMasker identification. The *Alu*J group consists of RepBase subfamilies Jb, Jo, Jr and Jr4. *Alu*S oldest contains RepBase Sp, Sq, Sq2d, Sx, Sx1, Sx3, Sx4, Sz, and Sz6. *Alu*S intermediate consists of Sg, Sg4 and Sg7. *Alu*S young contains RepBase subfamilies Sc, Sc5 and Sc8 (Jurka et al. 2005). Groups *Alu*Ta7, *Alu*Ta10 and *Alu*Ta15 do not contain additional subfamilies. Green, purple, blue and orange indicate lineage-specific subfamilies derived from the marmoset, squirrel monkey (shown here as 'squirrel'), owl monkey (shown here as 'owl'), and capuchin monkey (shown here as 'capuchin').

Alu subfamily phylogenetic analysis

A complementary Bayesian analysis of the evolution of these subfamilies was also completed. The *Alu*J portion of the Bayesian tree is generally in agreement with the RepeatMasker and network analyses (Figure 4.8, Figure 4.9, Table A4.2). It appears as though *Alu* subfamilies Jo and Jr are more closely related than previously thought, as subfamilies identified as Jo or Jr in the RepeatMasker analysis were grouped together in monophyletic branches (Figure 4.9, Table A4.2). However, it should be noted that Jo was generally the basal

group in a branching pattern (Figure 4.8, Figure 4.9). In addition, only subfamilies ascertained as lineage-specific from the marmoset genome were observed in this category.

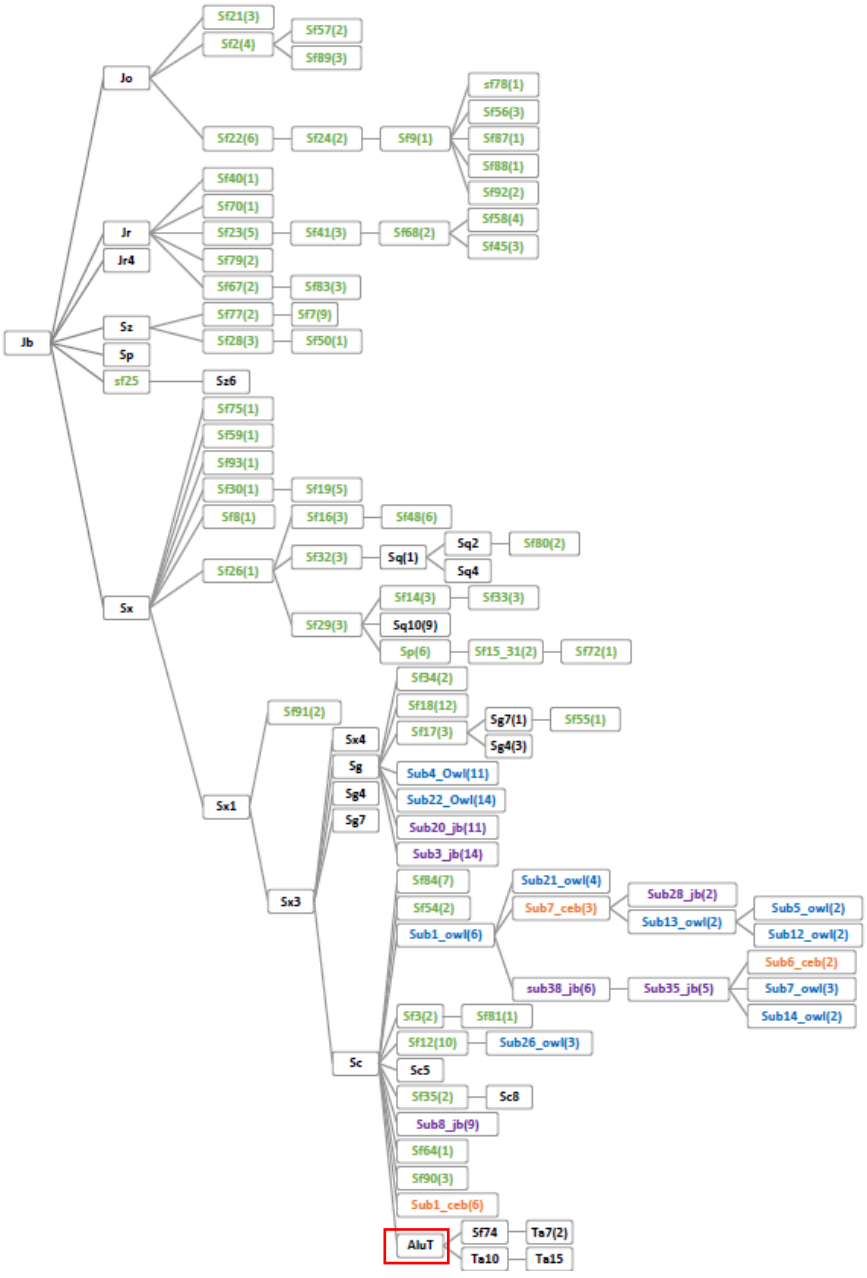


Figure 4.5. Network schematic of 189 *Alu* subfamilies. This network was generated using data obtained from RepeatMasker as well as informed by a multiple sequence alignment of all 189 subfamilies. Black lettering indicates a predefined subfamily obtained from RepBase (Jurka et al. 2005). Green, blue, purple and orange lettering indicates that subfamily was a lineage-specific marmoset, owl monkey, squirrel monkey or capuchin monkey subfamily, respectively. Numbers in parentheses indicate the number of mutations that occurred between the subfamily and its parent node. Boxed in red is a putative *Alu*T subfamily as the fusion event between an Sc and Sp element (Ray and Batzer 2005).

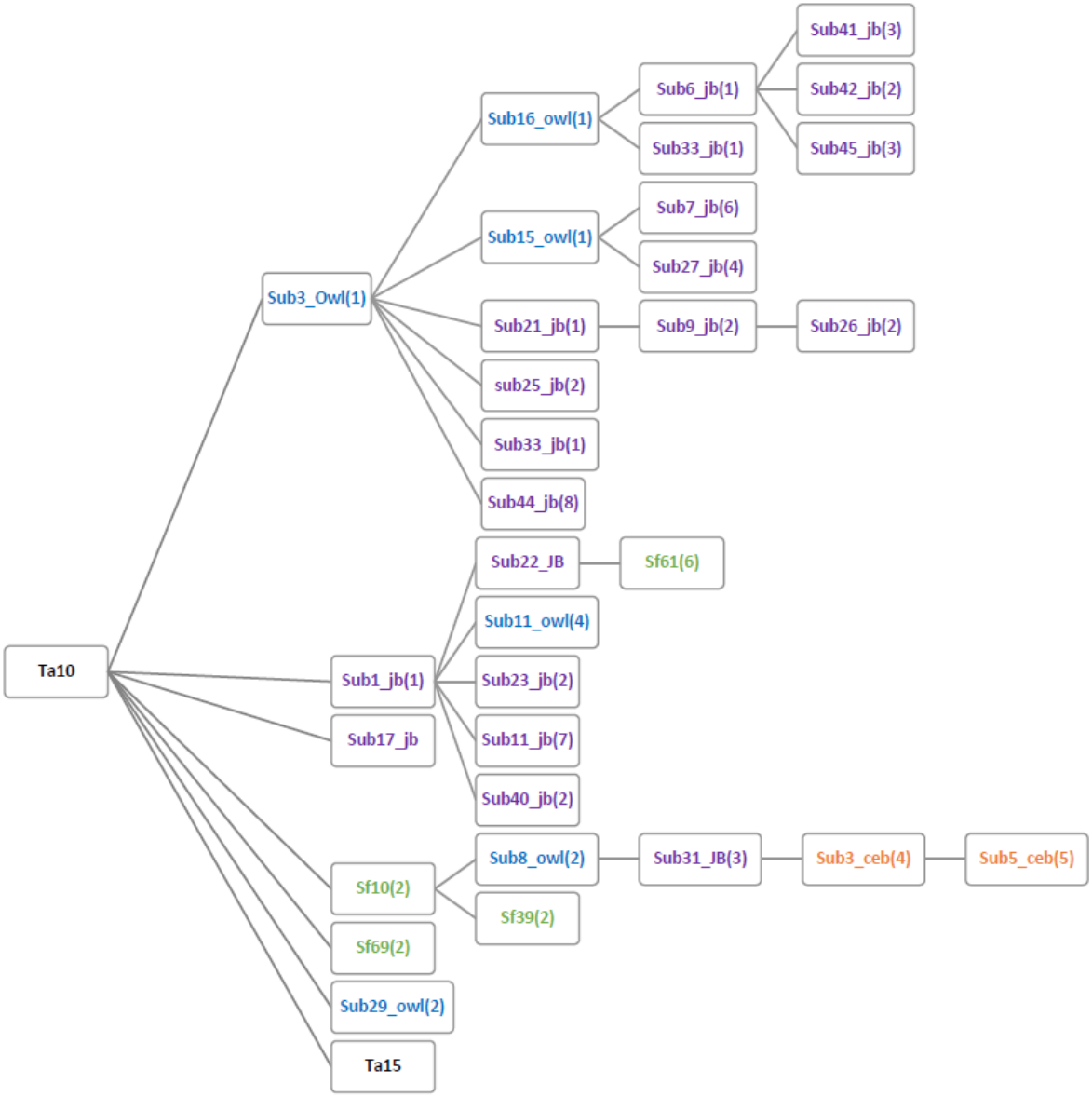


Figure 4.6. Network schematic of *Alu*Ta10 subfamilies. This network was generated using data obtained from RepeatMasker identifying subfamilies closely related to*Alu*Ta10 as well as informed by a multiple sequence alignment of all 189 subfamilies. It is a continuation of the network in Figure 4.5. Black lettering indicates a predefined subfamily obtained from RepBase (Jurka et al. 2005) or Ray and Batzer 2005. Green, blue, purple and orange lettering indicates that subfamily was a lineage-specific marmoset, owl monkey, squirrel monkey or capuchin monkey subfamily, respectively. Numbers in parentheses indicate the number of mutations that occurred between the subfamily and its parent node.

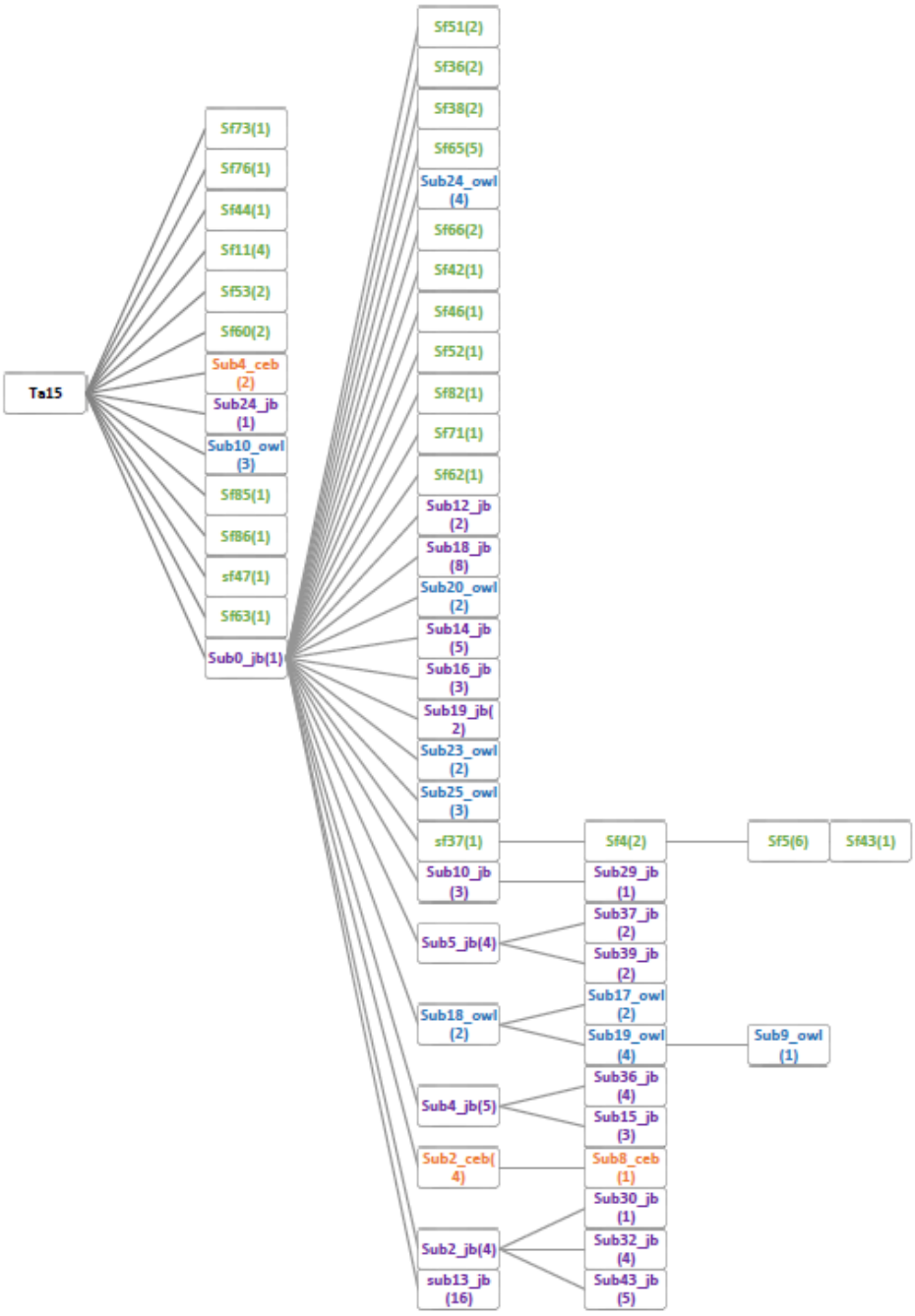


Figure 4.7. Network schematic of *Alu*Ta15 subfamilies. This network was generated using data obtained from RepeatMasker identifying subfamilies closely related to *Alu*Ta15 as well as informed by a multiple sequence alignment of all 189 subfamilies. It is a continuation of both Figure 4.4 and Figure 4.5. Black lettering indicates a predefined subfamily obtained from RepBase (Jurka et al. 2005) or Ray and Batzer 2005. Green, blue, purple and orange lettering indicates that subfamily was a lineage-specific marmoset, owl monkey, squirrel monkey or capuchin monkey subfamily, respectively. Numbers in parentheses indicate the amount of mutations that occurred between the subfamily and its parent node.

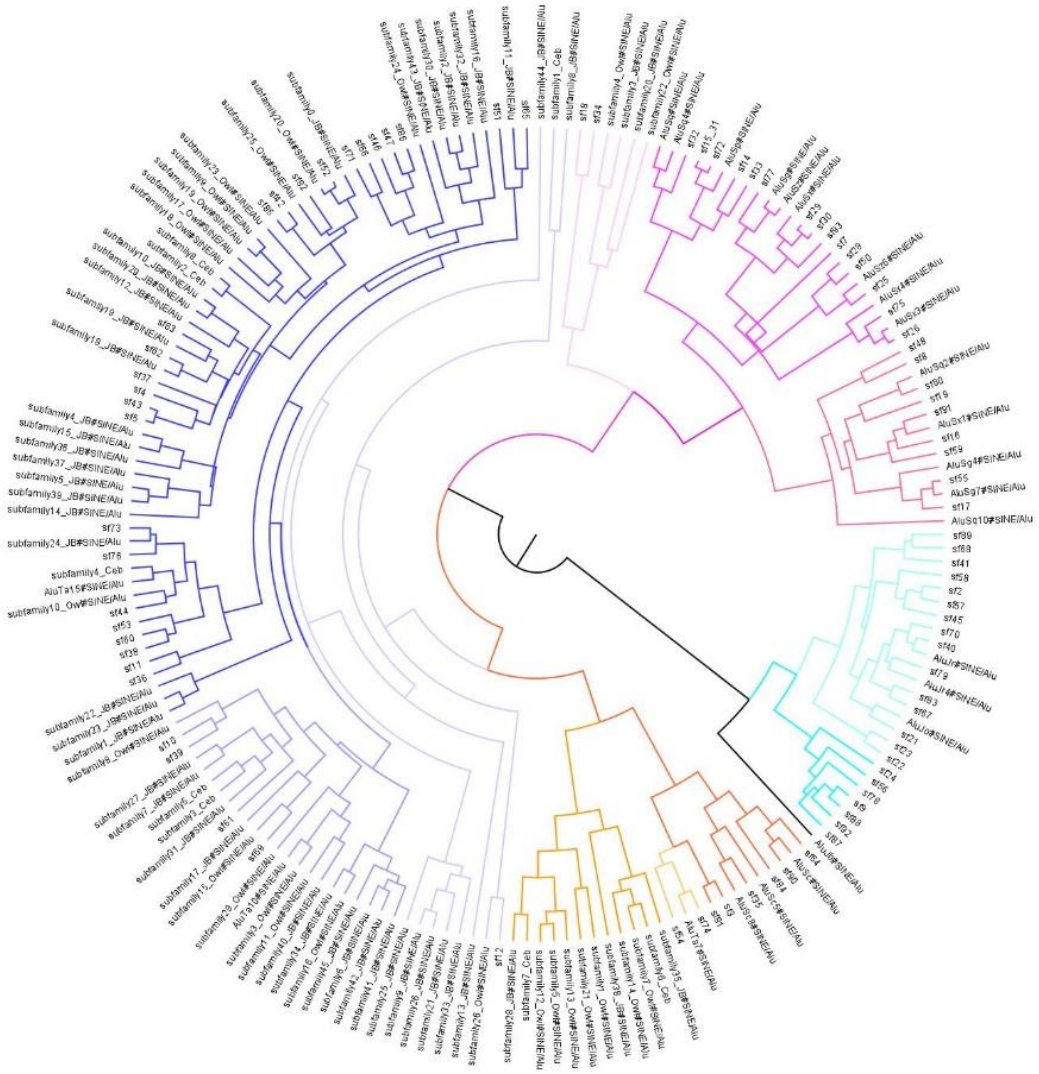


Figure 4.8. Bayesian tree of *Alu* subfamilies. This tree depicts the subfamily evolution of the 189 *Alu* subfamilies (See Materials and Methods). Labels that begin with "sf" are subfamilies identified in the marmoset genome (Worley et al. 2014). Labels that contain "jb", "ceb" and "owl" were obtained from the squirrel monkey (Baker et al. 2017), capuchin monkey and owl monkey, respectively. Teal indicates the *Alu*J branch, with darker shades indicating a basal branch and closer to *Alu*Jb, and lighter shades containing Jo and Jr subfamilies. Orange indicates the *Alu*Sc branch, with darker shades corresponding to those subfamilies identified as *Alu*Sc, with lighter shades those subfamilies with higher percent divergence values forming a separate monophyletic group. Pink indicates the older *Alu*S subfamilies, with darker and lighter shades depicting the separation of these subfamilies based on divergence values and general grouping. Purple indicates the *Alu*Ta10 and *Alu*Ta15 subfamilies, with the darkest shade belonging to the branch that contains *Alu*Ta10 with the lightest shades belonging to those subfamilies that form clades but do not form a group that contains the *Alu*Ta10 or *Alu*Ta15 consensus sequences. Black indicates the *Alu*Jb subfamily.

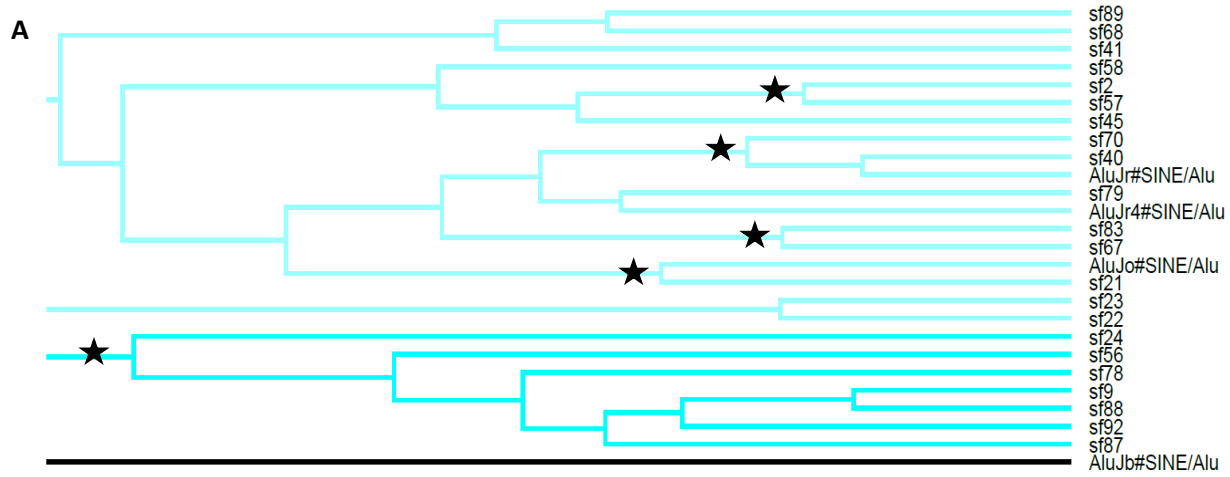


Figure 4.9. A closeup of the *Alu*J branch of the Bayesian phylogenetic tree (from Figure 4.8). Labels that begin with "sf" are subfamilies identified in the marmoset genome (Worley et al. 2014). All other subfamilies are derived from RepBase (Jurka et al. 2005). Black stars indicate group agreement with the network analysis.

When the *Alu*S portion of the Bayesian tree was analyzed, there is also agreement with the network analysis in terms of certain subfamilies forming a monophyletic group (Figure 4.5, Figure 4.8). In addition, there was a separation of *Alu*Sc from all other *Alu*S subfamilies (Figure 4.8). It was observed that subfamilies with a low percent divergence from the RepeatMasker identified consensus sequence were more likely to have congruent branching patterns with the network analysis, while higher divergence values from the RepeatMasker identified subfamily resulted in less agreement with the network analysis (Figure 4.5, Figure 4.9, Table A4.2). Subfamilies identified as *Alu*Sz formed a monophyletic group with the RepBase consensus sequence of *Alu*Sz (Figure 4.8, Figure 4.10). This same observation was made for *Alu*Sg7 and *Alu*Sp identified subfamilies. However, the Bayesian analysis and the network analysis did not match when comparing the Sx, Sx1, Sz, and Sq subfamilies in terms of branching pattern and grouping (Figure 4.8, Figure 4.10). This indicates that these subfamilies are potentially more closely related, making exact subfamily identification and branching difficult to determine.

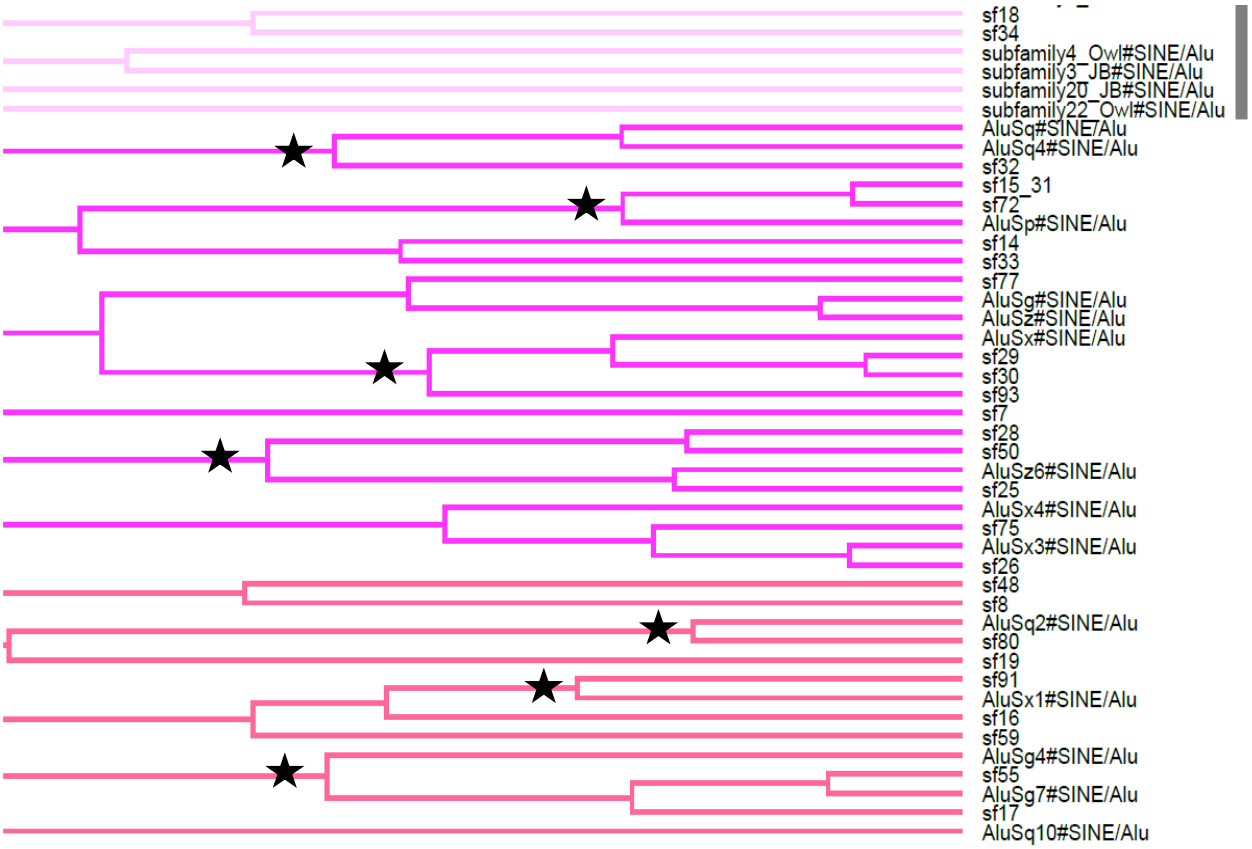


Figure 4.10. A closeup of the *Alu*S branch of the Bayesian phylogenetic tree (Figure 4.8) that includes older and intermediate *Alu*S subfamilies. Labels that begin with "sf" are subfamilies identified in the marmoset genome (Worley et al. 2014). All other subfamilies are derived from RepBase (Jurka et al. 2005). Labels that contain "JB", "ceb" and "owl" were obtained from the squirrel monkey (Baker et al. 2017), capuchin monkey and owl monkey, respectively. Black stars indicate high monophyletic group agreement with the network analysis. The grey bar indicates subfamilies with a higher percent divergence from their RepeatMasker identified subfamily.

Within the *Alu*Sc branch there was a further division into two groups: subfamilies identified as *Alu*Sc with lower percent divergence, and subfamilies with a higher percent divergence, a trend that was previously described for the other *Alu*S derived subfamilies (Figure 4.11). Subfamilies with lower percent divergence values belonged exclusively to the marmoset

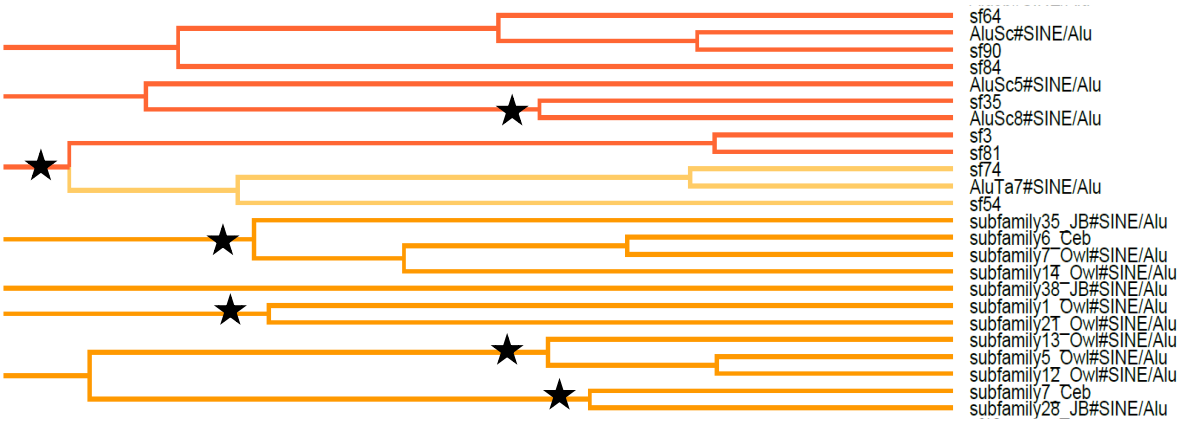


Figure 4.11. A closeup of the *Alu*Sc branch of the Bayesian phylogenetic tree (Figure 4.8). Labels that begin with "sf" are subfamilies identified in the marmoset genome (Worley et al. 2014). All other subfamilies are derived from RepBase (Jurka et al. 2005). Labels that contain "JB", "ceb" and "owl" were obtained from the squirrel monkey (Baker et al. 2017), capuchin monkey and owl monkey, respectively. Black stars indicate monophyletic group agreement with the network analysis.

derived dataset while higher percent divergence values typically derived from the remaining NWM, and formed their own monophyletic group (Figure 4.11). There are some groups that were congruent with the network analysis, su ch as the grouping and branching order of sub38_jb, sub35_jb, sub5_ceb, sub7_owl and sub14_owl (Figure 4.11). In addition, there is a close relationship between sf74 and *Alu*Ta7, which was placed in the *Alu*Sc group (Figure 4.11).

The *Alu*Ta10 portion of the Bayesian tree contained very few subfamilies (4) that originated from the marmoset genome, with general agreement with the network analysis (Figure 4.6, Figure 4.8, Figure 4.12).

The *Alu*Ta15 portion of the Bayesian tree is in agreement with the network analysis and RepeatMasker identification. The general trend in the *Alu*Ta15 branch was the presence of monophyletic groups belonging to a single taxa. It is interesting to note that the capuchin subfamilies subfamily8 and subfamily2 grouped with squirrel monkey derived subfamilies (Figure 4.13).

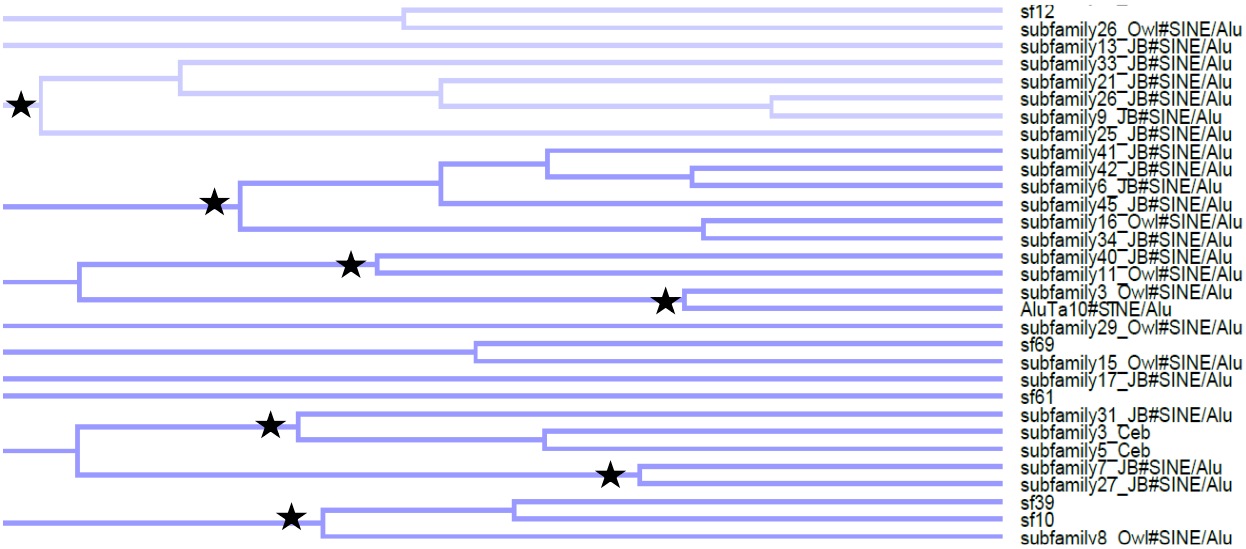


Figure 4.12. A closeup of the *Alu*Ta10 branch of the Bayesian phylogenetic tree (Figure 4.8). Labels that begin with "sf" are subfamilies identified in the marmoset genome (Worley et al. 2014). All other subfamilies are derived from RepBase (Jurka et al. 2005) or Ray and Batzer 2005. Labels that contain "JB", "ceb" and "owl" were obtained from the squirrel monkey (Baker et al. 2017), capuchin monkey and owl monkey, respectively. Black stars indicate group agreement with the network analysis.

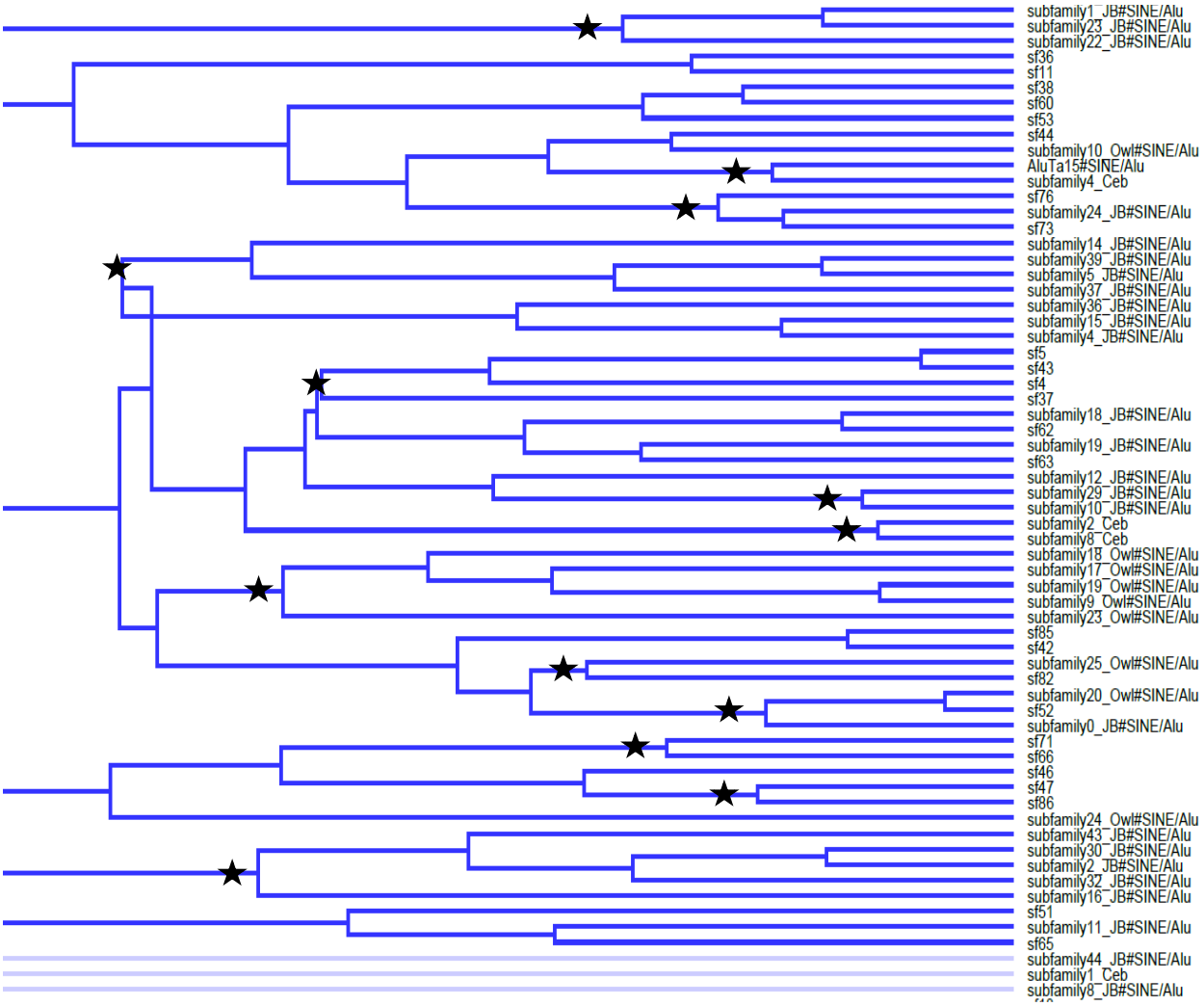


Figure 4.13. A closeup of the *Alu*Ta10/*Alu*Ta15 branch of the Bayesian phylogenetic tree (Figure 4.8). Labels that begin with "sf" are subfamilies identified in the marmoset genome (Worley et al. 2014). All other subfamilies are derived from RepBase (Jurka et al. 2005) or Ray and Batzer 2005. Labels that contain "JB", "ceb" and "owl" were obtained from the squirrel monkey (Baker et al. 2017), capuchin monkey and owl monkey, respectively. Black stars indicate group agreement with the network analysis.

Discussion

This study is the first attempt to complete a network of *Alu* subfamilies compiled from multiple data sets of closely-related taxa, and provide a framework to begin a standardized nomenclature that accommodates these large expansions of *Alu* element subfamilies. These data indicate that marmoset is the most basal lineage of the four NWM in this study, as only the lineage-specific insertions ascertained from marmoset included members that were derived from the oldest *Alu* subfamilies (Jb, Jo, Jr, Jr4, Sp, Sq, Sq2, Sq10, Sx, Sx1, Sx3, Sx4, Sz and Sz6). The lineage-specific insertions ascertained from the capuchin monkey genome were identified in the RepeatMasker analysis as belonging to younger subfamilies compared to the other genomes. This suggests that capuchin monkey is potentially a younger lineage than the three other NWM lineages in this study. The two intermediate lineage-specific subfamilies identified in squirrel monkey and owl monkey genomes suggest a similarly intermediate placement of these two families within the larger Cebidae lineage. The largest expansion of *Alu* elements in older, intermediate and younger *Alu* subfamilies occurred in the marmoset genome. This large expansion of *Alu* elements compared to other NWM genomes mirrors the activity of Platy-1 retrotransposable elements (Konkel et al. 2016; Storer et al. 2019).

These data show bursts of activity arising from the *Alu*Ta10 and *Alu*Ta15 subfamilies, in agreement with the bush-like model of *Alu* mobilization (Cordaux et al. 2004; Han et al. 2005; Ray 2007). The minimal differences between the *Alu*Ta15 consensus sequence and the large number of lineage-specific subfamilies from the marmoset, squirrel monkey and owl monkey genomes are seen in the few, at times only one, diagnostic mutation (Figure 4.5; Figure 4.6; Figure 4.7). This study also highlights the concurrent activity of multiple *Alu* subfamilies within each given lineage, similar to what has been previously reported for human specific *Alu*

subfamilies (Cordaux et al. 2004). This is also potentially why the network analysis and phylogenetic tree contained some differences. The diagnostic mutation accumulation may lead to a polytomy, which are avoided in a Bayesian analysis that forces bifurcation (Lewis et al. 2005). It is also interesting to note that in the *Alu*Ta15 group there is an absence of a hierarchical scheme of a lineage-specific subfamilies leading from one organism giving rise to another lineage-specific subfamily to another, as seen in *Alu*Ta10 (Figure 4.6; Figure 4.7). This provides support that *Alu*Ta15 derived subfamilies are the youngest group of expanding subfamilies within the Cebidae lineage as previously reported (Ray and Batzer 2005).

The alignment analysis of *Alu* elements ascertained from the marmoset, squirrel monkey, capuchin monkey and owl monkey genomes provide strong evidence of ILS. ILS is a product of the rapid speciation that occurred within NWM during which time a large number of *Alu* insertions remained polymorphic within the emerging taxa and became randomly distributed among the four lineages studied here. Extensive ILS results in incongruent phylogenetic trees (Schneider et al. 2001; Cordaux et al. 2004; Schneider and Sampaio 2015). The PCR analysis confirmed that each phylogenetically informative group is represented by having shared *Alu* insertions that were predicted in the alignment data sets. In addition, the sequence data present in the assembled NWM genomes provided higher levels of homology with which to unambiguously assign *Alu* insertions to a phylogenetically-informative group. This is in contrast with the minimal homology provided by SRA data alone (Chapter 3). Although not analyzed here, the alignment data also provides information on truncated *Alu* elements and near-parallel insertions (data not shown). Near-parallel insertions can obscure a phylogenetic analysis if not carefully considered (Ray et al. 2006). While shown to be rare in primates, precise parallel insertions are also possible to parse out with this alignment data set in combination with the *Alu* network

analysis. For example, the subfamily of a shared element between capuchin monkey and owl monkey to the exclusion of squirrel monkey and marmoset can be determined with this expanded subfamily data set. If the subfamilies of both *Alu* insertions from the capuchin monkey and owl monkey in the alignment are the same subfamily or closely related, it is more likely that this is truly a shared element rather than a precise parallel insertion. Alternatively, if the subfamilies from the capuchin monkey and owl monkey differ, it is probable that a precise parallel insertion took place.

The alignment approach also provided some evidence for resolving Cebidae NWM evolutionary relationships. Previous studies based on both morphology and retrotransposable element insertion presence have indicated a close relationship between the capuchin monkey and the squirrel monkey (Marroig 2007; Martins et al. 2015; Martins-Junior et al. 2018; Storer et al. 2019). The CS category contained the highest number of shared *Alu* insertions compared to any other combination of taxa based on sequence alignments. the data from the current alignment portion of this study is in agreement with previous research. In addition, out of the four possible combinations of elements that are shared between three NWM to the exclusion of the fourth, the COS group (*Alu* element shared between capuchin monkey, owl monkey and squirrel monkey to the exclusion of marmoset) is most highly represented in the data set with a total of 467 combined insertions. This grouping is in agreement with marmoset as ancestral to capuchin monkey, owl monkey and squirrel monkey in the subfamily network analysis as well as the alignment analysis that showed capuchin and squirrel monkeys have a high amount of shared *Alu* elements to the exclusion of owl monkey and marmoset. It should be noted that the categories and corresponding values in Figure 4.2 may contain overlapping information from the different genomes, i.e., the same insertion is represented twice. It is also possible that a few of the *Alu*

insertions are not in the proper category due to near parallel insertions. In addition, *Alu* elements that were truncated in the data set were treated as not present. Such truncations may be due to gaps in the assembly where *Alu* elements are difficult to uniquely place to one location in the genome. Future work on generating high-quality assemblies should be a priority, as highlighted by gaps and Ns (where the sequence quality was not high enough to assign a nucleotide) seen in this study. This effort may include generating high quality assemblies using a variety of sequencing methods, which may include long sequencing technologies such as PacBio (Rhoads and Au 2015) or NanoPore (Goto et al. 2019), in conjunction with Illumina sequencing (Buermans and den Dunnen 2014) and Hi-C sequencing (Belton et al. 2012). A combination of these methods have been used to reproduce fully assembled genomes or higher quality than previous versions, such as the gray mouse lemur (Larsen et al. 2017).

Using two complementary methods this study has provided strong evidence for a branching pattern that favors marmoset as the basal organism to the capuchin monkey, squirrel monkey and owl monkey. In addition, capuchin monkey and squirrel monkey are sister groups with owl monkey as an outgroup to these sister groups. The subfamily analysis has also provided a precedent to use repetitive elements within a lineage to inform a phylogeny and a framework to begin working on a new *Alu* nomenclature to accommodate the large number of subfamilies now available.

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Chapter 5. Conclusions

Retrotransposable elements, with an emphasis on *Alu* elements, have provided a wealth of information to elucidate primate phylogenies (Singer et al. 2003; Roos et al. 2004; Ray and Batzer 2005; Ray et al. 2005; Li et al. 2009; McLain et al. 2012; Meyer et al. 2012; Jordan et al. 2018). As neutral inhabitants in the genome they reside, *Alu* elements are ideal phylogenetic markers. The ancestral state is known, they are easy to analyze via PCR due to their small size, and they are nearly homoplasy-free compared to other markers such as SNPs (Ray et al. 2006). *Alu* element presence and/or absence can be used to determine branching order in a phylogeny. In conjunction with the aforementioned parsimony analysis, an analysis of *Alu* subfamilies can also provide phylogenetic information (Ray and Batzer 2005). If the evolution of *Alu* subfamilies is known, the *Alu* element subfamily content of a given genome in comparison with others should be able to inform a phylogeny.

The amplification of retrotransposable elements in different genomes can provide evidence for close or alternatively, highly diverged relationships as well as the tempo of mobilization. In Chapter 2, the amplification of retrotransposable element Platy-1 was assessed in four NWM genomes: marmoset, capuchin monkey, squirrel monkey, and owl monkey. Although ~2300 full-length Platy-1 elements representing 62 subfamilies were initially found in the marmoset genome (Konkel et al. 2016), the three other NWM genomes did not have this same level of Platy-1 mobilization. Only a small number of Platy-1 elements, in comparison to marmoset, were ascertained from the owl monkey, squirrel monkey and capuchin monkey genomes, with all of the lineage-specific Platy-1 elements fixed within the squirrel monkey and capuchin monkey populations. Evidence for on-going Platy-1 amplification in the owl monkey was shown with two new Platy-1 subfamilies and 31 polymorphic Platy-1 insertions. Future

work with other Callitrichinae, such as tamarins, may provide clues to the apparently large gap in activity within the Cebidae lineage between the marmoset and owl monkey, capuchin monkey and squirrel monkey genomes. However, future work will not use Platy-1 elements to elucidate the controversial NWM phylogeny, as the majority of the few elements ascertained from the owl monkey, squirrel monkey and capuchin monkey were shared.

The shortcomings of the Platy-1 element can be made up for in *Alu* elements. Although only a few hundred Platy-1 elements were discovered the owl monkey, squirrel monkey and capuchin monkey genomes, *Alu* elements are prolific. Hundreds of thousands of those copies are full-length *Alu* elements. The hypothesis was that with this sheer volume of *Alu* elements, the factors confounding the resolution of the NWM phylogeny, such as ILS as the results of rapid speciation and ~20 my of divergence as species, would be overcome. Chapter 3 explored a computational pipeline, polyDetect (Jordan et al. 2018), to analyze shared *Alu* elements among four NWM, marmoset, capuchin monkey, owl monkey and squirrel monkey, from publically available short read data. The polyDetect pipeline performs two sequential mapping steps, first of the short reads to the *Alu* consensus sequence, and second of the flanking sequence to a common reference genome (Jordan et al. 2018). Although useful in resolving the baboon phylogeny, the ~20 my divergence confounded the data, with few *Alu* repeats detected in the output as a result of insufficient homology of the short reads.

In addition, it was also determined that the reference genome used greatly influenced the phylogenetic tree. Differing branching patterns were observed when two non-Cebidae NWM genomes were utilized, although these genomes produced the same result with high bootstrap support. High homoplasy statistics for all trees drawn prompted a closer look at the polyDetect output. An extraction of the FASTA sequence from the polyDetect output reference genome

coordinates and sequent alignment of orthologous sequences indicated that the majority of the predicted insertions were in fact shared by all four NWM tested. Analyzing the alignment data of the first step of polyDetect indicated no issues with mapping the short reads to the *Alu* consensus sequence, but did suggest that the subsequent mapping of the reads uniquely to the reference genome was difficult. This is potentially due to the A-rich TSDs, which may obscure accurate mapping (Szak et al. 2002; Konkel et al. 2015). An attempt to overcome this limitation by adding a filter to only keep those reads that contained 30 bp of 5' flanking sequence was not beneficial to this study as longer stretches of sequence identity are required to accurately resolve the NWM phylogeny.

Chapter 4 analyzed *Alu* elements extracted from the four aforementioned NWM genomes with 600 bp of flanking sequence on both the 5' and 3' ends of the TE. The 1200 bp total of flanking sequence allowed for an accurate alignment and assessment of shared *Alu* insertions that might inform the NWM phylogeny. An assessment of the alignments determined that all combinations of potentially phylogenetically-informative *Alu* loci were observed. Additional analyses via PCR confirmed that every phylogenetically-informative category of shared *Alu* insertions was present. However, two groups had higher amount of shared *Alu* insertions than others: CS (shared between capuchin monkey and squirrel monkey and absent in the marmoset and owl monkey genomes) and COS (shared between capuchin monkey, squirrel monkey and owl monkey genomes and absent in the marmoset genome).

A complementary *Alu* subfamily analysis was also completed. 189 subfamilies combined from lineage-specific *Alu* subfamilies ascertained from the marmoset, squirrel monkey, owl monkey and capuchin monkey genomes were analyzed with a network analysis and aligned to complete a Bayesian phylogenetic tree. General agreement was observed between both analyses,

and a hierarchy of *Alu* subfamilies emerged. Only marmoset derived *Alu* subfamilies were closely related or derived from the oldest *Alu* subfamily J and the oldest of the *Alu*S subfamilies, while squirrel monkey and owl monkey derived subfamilies began to populate the intermediate and younger *Alu*S groups. Capuchin monkey derived elements were only observed in the youngest *Alu*T type elements. This data is consistent with the alignment analysis in the first part of chapter 4 that found the two highest categories as those *Alu* insertions shared only by capuchin monkey, squirrel monkey and owl monkey. In addition, the discovery of the category with the highest number of insertions shared between capuchin monkey and squirrel monkey is in agreement with previous analyses of this close relationship (Marroig and Cheverud 2004; Martins et al. 2015; Martins-Junior et al. 2018; Storer et al. 2019). Future studies will use the network analysis and Bayesian phylogenetic tree to take a second look at the nomenclature for *Alu* elements so as to accommodate the discovery of a large number of new subfamilies.

These studies highlight the versatility of retrotransposable elements Platy-1 and *Alu* as homoplasy-free markers to inform the tempo of TE amplification in a diverse set of organisms. It is hoped that this work can inform future research in the following ways:

1. To use caution and know the limitations of a computational pipeline when applied to their data and how the accuracy of their results can be improved.
2. How to use the amplification rate of lineage-specific retrotransposable element insertions as a comparison between organisms, potentially highlighting differences between species.
3. To use the framework provided here in the form of a network analysis and Bayesian phylogenetic tree to inform phylogenetic analyses using retrotransposable elements.

4. Create a new *Alu* nomenclature system that can accommodate the large number of subfamilies recently discovered.

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Appendix A. Supplemental Data

Chapter 2

Table A2.1: Lineage-specific Platy-1 capuchin monkey primers

Locus	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')	Filled (bp)	Scaffold	Start	End	Strand	Platy-1 Subfamily
CC_3	ACATATGACAGTGGGGATGGA	CAAAGAAGACTTCCCATCACTG	370	NW_016107319.1	11900622	11900726	-	4a
CC_5	TCTGGATTTGGTGATCAGGAG	AGATTTGCAGACACCACTGCT	385	NW_016107374.1	7094536	7094634	-	4a
CC_7	CACTTGGAACATTTCTGCCC	AGAGACAGGCCTTTTCCCTTA	401	NW_016107500.1	3906202	3906304	-	4a
CC_8	TGTCAGCAACCATCTATGTCC	AGGATTCCTGATCAACAGTAGC	349	NW_016107649.1	962501	962603	-	4a
UU_Ceb_1_Redo	GGTGGAGACCCCTTACAGTTT	GTTTCCTCAGTGCCTAGCAGA	595	NW_016107324.1	6877109	6877213	+	4a
Ceb_2	GTAAGGAAGCAGGGATTCTCA	TTGCTAGGTATTGCCAACTTG	214	NW_016107365.1	7945868	7945971	-	4a
Ceb_4	CCCAATTTCCCTTTCCTGT	CCCTGGGCTAGGTACAGTCA	276	NW_016107408.1	6305816	6305918	-	4a
Ceb_5	TTCTGTCCCCAAAGTGGTTAC	CAAAATTAGAGCCAGGCAAAG	254	NW_016107435.1	3016219	3016320	-	4a
Ceb_6	CTTGACACCAAAGGCACAACC	GATCTCCAGTTTCATCCATGC	305	NW_016107564.1	797100	797202	-	4a
Ceb_7	GGCTGCCATAAATAACCTATCC	TAGGCTCAGGTTTGCATCTG	320	NW_016107774.1	1415826	1415928	+	4a
Ceb_8	TGGTTGGAATAATGGAAGCATG	AGGGCTAAAGGCCACTAACTT	284	NW_016107952.1	705047	705154	+	5
Ceb_11	TGCTGGTAAATAGGTCACAGTAGTTG	TTGCCACCTAAGGGAAGTCTT	635	NW_016107350.1	542274	542376	+	4a
UU_Ceb_13_Redo	CCTAAGGCTGGGAGTTTAGGA	TTGGCCAGACTGGTCTCAAT	242	NW_016107512.1	657003	657084	-	3
U_Ceb_Platy1-4_1	CCTGTTAATGCTCTTTAGTACATTGC	GGAAGTTTCCCTCTATTCTTCATTT	299	NW_016107564.1	562265	562368	+	4
U_Ceb_Platy1-4a_21	CCCATGACAAGAGCCAAATA	TCAGTGTGGTGTTGAAATGC	494	NW_016107707.1	959430	959531	+	4a

U_Ceb_Platy1-5_23	CCAAAATAGAGTGTATTAAAAGCACAG	CAGTACCTACATTGGTAAGCACATC	289	NW_016107831.1	219785	219890	+	5

Table A 2.2 Lineage-specific Platy-1 squirrel monkey primers

Locus	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')	Filled (bp)	Scaffold	Start	End	Strand	Platy-1 Subfamily
Ply4a-8	GTGGCTTACATGAGTGGAAG	GCCAGTGCTTTGGTGTTGTA	270	JH378105.1	36625740	36625839	+	4a
Ply4a-10	CTTTCCCAGTCCTCTGGCTA	GTCCTGCCTTGGTCTTTCTG	331	JH378300.1	443982	444083	+	4a
Ply4a-16	AGTTTGAGGCTGCAGTAGGC	CCAGGATGCCCATAATAAGC	285	JH378142.1	1163397	1163500	+	4a
Ply4a-17	TGAGCCCTGCTCAGTTCC	GGGAGCAGTGATTTCTGAGC	465	JH378115.1	352706205	352706305	-	4a
Ply4a-21	TCCGTTGAGATGTCTGTTGC	CGTTCCCAAACTTGAGAAAGAT	337	JH378107.1	429061661	429061765	+	4a
Ply4a-25	CCACCATGGCATGTGTGTAC	AACTGACTTGCTCGCTGTTT	356	JH378286.1	138594	138597	+	4a
Ply4a-27	GGGTCCATCAACTGGAAGAC	ATGCCGTTACTGCCACATCT	355	JH378155.1	1183493	1183596	+	4a
Ply4a-30	TATGACTGGGCCATGTTTCC	GGAGCTCATTCATGTCATTGC	341	JH378149.1	163700438	163700541	-	4a
Ply4a-34	GCTTTGCACCTCAGCTCCTA	AGCAATTTACAAAGGAATATATGCAG	592	JH378173.1	66666581	66666683	-	4a
Ply4a-37	CACCTGCTGCTTGGGTAGAT	GCTTAGTGTGATGCTTGGCATA	350	JH378107.1	678206232	678206334	-	4a
Ply4a-46	GTCAACTCAGAATTCTTATCCAGTG	ACCTTTGCATCTATTTACCTTCCTC	492	JH378111.1	400603717	400603820	-	4a
Ply4-1	AAGATGCTCAACTTCACTAACAGAAT	TCCTTTGCTGTTTATCAAGAACA	554	JH378181.1	136600588	136600683	+	4
Ply5-12	AGGAGCAGTCAGCGTAAATG	CTATCATCAAATCCTGTCTCTGCT	541	JH378115.1	141902187	141902292	-	5
E_30	TTCTCAAAACGACCCTGACA	CTGGAACGAGAAGCCAATACA	380	JH378113.1	394708956	394710257	-	4a
E_31	GCTAGCAAGACTGCCTTCAAA	TCTGCTTTCCCTTTCTGACTG	785	JH378119.1	305806949	305808244	-	4a
E_32	CATCCTCCTGTCCTGGAACTT	GCTCCAAGCCTGCAAGATGA	285	JH378122.1	111800851	111802155	-	4a
E_38	GGCTAGAGTTTTCGACAAGAGC	GTGCTTGGCTTATCTCGCTTA	377	JH378193.1	428100387	428200691	+	4a
E_43	GGAAGGCAGGGTTGTTTACTC	GTGCCTTTCAAACCAGTCTCA	462	JH378276.1	529891	531191	+	4a
E_45	CACCATTGTAATGAAATGCCATCAT	CCTTGTTTCTGAGGAAGATTCAA	251	JH378282.1	184332	185635	-	4a

Table A2.3 Lineage-specific Platy-1 owl monkey primers

Locus	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')	Filled (bp)	Scaffold	Start	End	Strand	Platy-1 Subfamily	New Subfamily designation

U_OM_72535	GCTGGAAAATTCCAAGCAA	GCAAGTTTTGTAGGTTTCATGC	370	NW_017217255.1	17438	17540	+	4	4b3
U_OM_87201	CAAATCTTCGTCTGCCATTTAG	TGTGGCTGTGGAAATCATTAG	318	NW_017218720.1	32896112	32897144	-	4	4b3
U_OM_87757	AGCCTTATTGCTGGTATGCAG	CATGAAAAACCTGTGGTTTGG	316	NW_017218775.1	61978333	61979333	-	4a	
U_OM_67868	AACTCAGAGAAGAGGTCAAGCA	CATCCAAACAGCTCTTGCTAA	404	NW_017216786.1	67789441	67790433	-	4a	
U_OM_69313	TGTTGGCCAGGATGGTCT	GGTCAATTTGGACATCAACATC	500	NW_017216931.1	30481133	30482155	-	4	4b
U_OM_90080	CCTGGCTCTTTTTCTTTCTTTC	AGTTCAGAGCAGGAGTTGAGG	249	NW_017219008.1	706	808	+	4	4b
U_OM_73758	GGCCAGTACCATACTGTCTCAA	CATAAACATGCCAGAAATGTCC	630	NW_017217375.1	328227	328329	-	4a	
U_OM_79090	CTTCCCTCTGTTCCAATTATCA	GGAAGGGTCCTAATAATGCCTA	391	NW_017217909.1	438815	438917	+	4	4b
U_OM_80979	AACAGTCATCCCAGACCAGTG	CATTATTTCGGCCCATGAA	380	NW_017218097.1	31643133	31644155	-	4	4b3
U_OM_73201	AGATGGTGCCAAATTGTTCTC	AGATCTTGGAATGACCAGTGC	395	NW_017217320.1	4719503	4719604	+	4a	
U_OM_83869	CTTCAGGGAGGGAATGTTCTA	TGTGTCAGGAGAATGGTTGTC	480	NW_017218386.1	10417195	10417299	-	4a	
U_OM_85757_v2	TGAGTGATAGAATTTGGGGAGA	CTGAATGTCTGTTAAGGCTTCC	897	NW_017218575.1	12425680	12425782	-	4a	
U_OM_84269	TGGGGGCTGAGACTATTAGG	TTTCCCTCCAAACGGTCATA	???	NW_017218426.1	121958	122061	-	4a	
U_OM_71126	TCTGGGACCAGATTCAATGA	GATCACAGGGTTGCAAACATT	???	NW_017217112.1	2521	2623	-	4a	
U_OM_71201	ACTAAGAAGCACGAAGGCAAG	CTCTCCTTCTAAGACCTTGTCAG	370	NW_017217201.1	132016	132118	+	4a	
U_OM_85913	CCCAGTGAGTTTGCTTTGAA	GCAGGGGTGGCTCTTAATAAT	435	NW_017218591.1	188266	188368	-	4a	
U_OM_79424	AGATGCATTTGGTCCTTTGAG	CGTGACCTAGGGCATGTTACT	534	NW_017217942.1	225694	225796	-	4	4b
U_OM_86114	CAGAGGGAAACCATTTTGTTG	GGCAGAAGAATTGCCTGAAC	465	NW_017218611.1	246267	246369	+	4a	

U_OM_76313	GAAGAAAGCGTTTGTGTCCAT	CTGGGCAACAAGAGTGAAACT	???	NW_017217633.1	304188	304290	+	4a	
U_OM_84436	GAGGCTACAGTGATGCATGGT	TCTCTCCCTTTCCCACCTC	273	NW_018443436.1	20312	20414	+	4	4b
U_OM_81312	GCCACATGTTAGTAGGGGATT	TAGGGGCTGCCATACTGAAC	518	NW_018131312.1	921455	921555	-	4a	
U_OM_84513	GAGGGGGCAAATTCTACAAA	TCATGTTCACTTATCCCTCTGG	704	NW_018451453.1	800595	800697	+	4	4b
U_OM_83802	GACTGGGAATGCCTAGTGCT	CCCAGAATTCCTGGATTCAA	593	NW_018380382.1	781164	781267	+	4a	
U_OM_89423	CAGGAAGGAGAGATTGACAGG	GCCTTCTCACATCCAGTAGGT	427	NW_018942943.1	1089486	1089588	+	4	4b
U_OM_81868	GCCTGACAGACCCTGAGTG	GTGCTAATACGGTGGCCAGT	365	NW_018186868.1	318750	318852	+	4	4b
U_OM_83813	CTCTTGGCTTTTCACCTTCTG	AGGCTGAAAAGTTTAAGGATGG	286	NW_018381383.1	552683	552786	-	4a	
U_OM_85957	GCTCATATGGTTTGTGACCTTT	CCCATGGTAGCTCAAGAAAAA	394	NW_018595957.1	947992	948094	+	4a	
U_OM_89979	TGCCTGGCAGTTGGTCTA	CAGAGAGTGGAGGGCGAGT	335	NW_018997949.1	1974646	1974750	+	4a	
U_OM_73423	CACTGATAGGTGCCAGAGGTA	TTAACCTCCCATTCCCATTG	316	NW_017342373.1	600379	600482	+	4	4b
U_OM_85458	TTTTTGGGGTGACAAAAGTGT	TCATTTTGGACGAGATGTTCA	299	NW_018545458.1	2034965	2035067	-	4a	
U_OM_66202	AACAGCAAATAGCCTCAGAAACA	GGTCTGTTCTTTTGTTTTTCTCC	345	NW_016620621.1	2027849	2027948	+	4a	
U_OM_89201	ATTTCCTTCCTCTCCTGTGGT	GGTATGGTAGCAGGTGCCTAT	460	NW_018920611.1	1245382	1245484	-	4a	
U_OM_76646	AGGCAAATATGGCAGAATATCA	AAATTCTTCAATGGCTTCCAAA	333	NW_017664676.1	1884707	1884807	-	4a	
U_OM_78901	GCCTTTCTCTCATTTTGCATT	TATCTGTTACATGATGGCTGACA	474	NW_017809011.1	1955069	1955170	+	4a	
U_OM_85202	CCAGGCCTTAAGTGATATACCC	AATTGAGCCACACTGGGAGTA	454	NW_018520202.1	276799 2	276809 4	+	4	4b3
U_OM_76757	CACAGATAATCTCCAAGGGTCTT	GTACAATGCGCTTGAGAGGA	504	NW_017675771.1	2674742	2674841	-	4a	

U_OM_91312	CATGGATGGTTGGAAATCACT	GATCTCTCAGGCTCAAGCAAT	450	NW_019191312.1	24183511	24184533	-	4	4b
U_OM_64424	AGACCAGAGGAAGTGGAGTTG	TGAAGAAGTCAGGAAGCTTGA	464	NW_016442441.1	23745011	23746044	+	4a	
U_OM_67424	CTGGCTACAGAAATGAGTGTCC	TCTCCACAAGTAGCGAGATGA	434	NW_016742441.1	22263136	22264166	-	4a	
U_OM_84424	TTGCAACTAGCCAATGAAGTG	GGCCCATGTACACCTATGTAA	552	NW_018442441.1	30538399	30539411	+	4	4b3
U_OM_73536	GGCATCAAGAGGCTGTCAC	GCATCTGGCAAGAAAGCATA	490	NW_017353616.1	28382788	28383900	+	4	4b
U_OM_84147	CCTGTGGCCCAGTCAAGT	TGATCGTCTCTTCATGTTTCTG	482	NW_018414717.1	35633339	35634422	-	4a	
U_OM_84902	CTGAGCCTCAAATCAGCAAA	CGATTCTCCTGTCTCACCTTC	600	NW_018490241.1	57224	57234	+	4a	
U_OM_68979	CCAGGCTGCTTAAAAGTATGAA	CAAGTGGAACTCCATGTATGATG	583	NW_016897941.1	43543266	43544288	+	4	4b
U_OM_66646	CTTTCCAGCTATTTGACCCTTT	CAAATTAGCAGCAAAGTGAACC	554	NW_016664661.1	37293355	37294377	-	4a	
U_OM_82979	TGAGGACTGAGTGAAAGAGCA	CTTTGTCCAGCTTTTCCATGT	370	NW_018297941.1	13324744	13325776	-	4	4b
U_OM_63980	CCCAGATGGCTTCAAAAATA	CACTCAGGATCTGGAGTCAGAA	409	NW_016398601.1	12473800	12474822	-	4a	
U_OM_83824	ACCCTGTCTCAAAATGCAAAG	CATGTGGAAAGCCTGGAGA	277	NW_018382841.1	11018500	11019522	-	4a	
U_OM_75646	CATCCACACGCTAGTACTGCT	CCTGAATAATGTCATCAACTGG	370	NW_017564661.1	44121522	44122554	-	4a	
U_OM_68646	GCAAACAGTAGCAACAATTTCA	TGGAATGCAGTGACTATTCAAA	566	NW_016864661.1	15046855	15047887	+	4a	
U_OM_85646	TGGAGGAAAAATTTGGATAGTCA	TTTGCAGATATTTTCCTCCAGTC	424	NW_018564661.1	14927200	14928222	+	4	4b
U_OM_91090	TGCATATTGCTTAATTGCTTTTC	TGACTTTAAAACCACTGTCCAAA	441	NW_019109901.1	14735433	14736444	+	4a	
U_OM_68313	TTTGCTGACTCACATCAATCTTC	GCCCATTTGGACAATATTTTATG	479	NW_016831331.1	14400755	14401773	-	4a	
U_OM_80424	GCCTAAAATTAACGTATGCCACA	CAACAACTCCACGATTTTCAA	360	NW_018042441.1	18292039	18293066	+	4	4b

U_OM_67202	CAAAGGTAGACGGTCATTTGC	GCCTAAGTTGCGATGTTCTTT	385	NW_016720 2.1	499159 8	499170 0	+	4a	
U_OM_62647	TGGTTATCAACTGGGAAGGTT	AAAATCCTAACATGCCACCAC	293	NW_016264 7.1	534356 5	534366 4	+	4a	
U_OM_91423	GTTGAAACCAATGACCCTTTG	TCCGGAAGGCATTACATTTAC	543	NW_019142 3.1	546374 39	546384 1	+	4a	
U_OM_71312	AAATTGCTATCCAAGGCACAG	TTATCAAGCTGGAGACCCAGT	356	NW_017131 2.1	553993 1	554003 3	+	4a	
U_OM_84868	TACCCTTCATCCACCCATATC	GGGGGACTGTTTTTCATTTTC	366	NW_018486 8.1	557516 9	557527 1	+	4	4b3
U_OM_86091	ACAGTCTCATTTGCAAGAGCA	AGAGGCCTAATTTGCCTTTTG	407	NW_018609 1.1	635139 7	635150 0	+	4a	
U_OM_91201	GGGGAATGATAGGATTGTTCTAC	GACTAATGCTGTTGGGCATCT	454	NW_019120 1.1	636790 2	636800 4	+	4	4b
U_OM_62869	TGTGGGATTCCAGAAAAAGTC	TTCCTGTTTTTCATCTCCTCCT	466	NW_016286 9.1	638185 8	638195 9	-	4	4b
U_OM_74202	TGGGTAGTGTGATACCTTCAGC	GAAATAAAACCACACACCAGCA	393	NW_017420 2.1	644678 0	644687 7	+	4	4b
U_OM_88312	GCTGAGGCATGACACTCACT	CTTGGCTGACAGAACAAGGA	117	NW_018831 2.1	649009 0	649019 2	-	4	4b
U_OM_64646	AGCCATGATTTAAGGCTCTTC	CCAGCTCAGCTCTGTCTACTG	115	NW_016464 6.1	963034 3	963044 5	-	4	4b
U_OM_86535	GCATATTCCCTGTGGAAAGAA	TTGAACCCTTCAATGGATTCT	134	NW_018653 5.1	970782 3	970792 6	+	4	4b
U_OM_84313	CGATCTGGGATTAACATTTCC	CTAATCCCATCTAGTGATGTTGC	118	NW_018431 3.1	998524 1	998534 3	-	4	4b
U_OM_87313	CAGTGTGTTACTGGCATAAGGA	GTATTCTTGGCCACCCTAAAA	124	NW_018731 3.1	100104 11	100105 13	+	4	4b
U_OM_85313	CACATAGCAATTGCCCAATAC	GTTTTAGCAGCTCCTCCTTC	118	NW_018531 3.1	107771 59	107772 61	-	4a	
U_OM_82423	ATCGGCAAATGGATTTAAGC	AGAGATTGAGCCACTGCACTC	110	NW_018242 3.1	109349 58	109350 60	-	4	4b
U_OM_74646	GCTCATGCCAATTACACCAGA	AGCAGATGTGAAAACTGAGCTG	112	NW_017464 6.1	110197 55	110198 57	-	4a	
U_OM_86901_v2	TGAGTTCTGGTTTGACTTTGG	AAGCTTTGGGTGATTAGATGG	121	NW_018609 1.1	113091 37	113092 39	-	4	4b

U_OM_66868	ACAGGGCCAGTATTCAAAGAT	AGCCCACTGGGTTTAATTTAG	125	NW_016216686.1	15675498	15675600	-	4	4b
U_OM_90534_v2	CCTCAAATGCTTGAAACTCCT	AGGTTGGTCTTGGACATTCAG	121	NW_016219053.1	17651049	17651154	-	4a	
U_OM_72423	GCTTCTCTTACTGGCCATCTC	TGTGTGCATCTATGTGTGTGC	111	NW_016217242.1	14359169	14359271	+	4	4b
U_OM_85657	AAGGCTGAGGTCTTTGGTCTT	TTGCTAGATCCTACCCCAGAG	124	NW_016218675.1	11668553	11668655	+	4a	
U_OM_73534	GAGGATTGCAGTTCAACATGA	GCCAGCAGATCCTTTATCTGA	120	NW_016217353.1	26052140	26052242	-	4	4b
OE_2	CAGAAGATCCAGGCTGCAGTA	AGGAGAGGAACCCTCCATTCT	400	NW_016216953.1	1490323	1490425	-	2	
OE_3	AGCAGTGCGGAACAAACTAA	TGTCCCTACATAGGACGCAAA	472	NW_016218400.1	1762727	1762828	+	2	4b
OE_6	TTGAGCTTCCTACCACAGAATC	ATTAACCTAGCCATCATCTCAC	308	NW_016216275.1	25726048	25727077	-	4	4b
OE_7	TCACTGAGCCTCTTCCTCTTG	AAGAGAAACATGAGCATGCAG	450	NW_016216353.1	25304002	25304104	-	4	4b
OE_8	TTCAGTTTCCTGGTCCTGATG	GCTATTGCCTTTCCTTTTCCA	285	NW_016216353.1	82979845	82980866	-	4	4b
OE_9	TATCCTTTTCACTCTTCCCCA	TGATTTATCCCCTCCTCCAAG	437	NW_016216364.1	63669976	63670988	+	4	4b
OE_10_v2	TTGCAGTGAGCAGAGATTGTG	GATCTGGTCGCCTACAATGAA	373	NW_016216392.1	59655	60666	+	4	4b
OE_11	GAGGCAGGAGAATCACTTGAAC	TTGTTCCCCAGTGAAGAGATG	292	NW_016216575.1	57038336	57039339	+	4	4b
OE_13_v2	CACATGGGAATTCAAGATGAGA	GGGTGGTGGTTACATGAGTGT	470	NW_016216842.1	43269754	43270754	-	4a	
OE_16	ATGTGAGCTGGCGCAGATA	TCTGCAAACAGCCTGCTTAAC	261	NW_016218131.2	30429633	30430635	-	4	4b3
OE_19	TCTTCTCCCTCCACTTGTTCT	CTGGGGTGACATCCTTGAA	250	NW_016218515.1	10054551	10055553	-	4	4b3
OE_22	CATGGTGAAACCCTGTCTGTAA	GAGGGTTAAGGTGGTTTGACT	316	NW_016218620.2	11158330	11159331	+	4	4b
OE_23	CAGCCCTTTTCTCTCTTCATCA	TTAAAATGGTTCATCCCCTGT	283	NW_016218848.1	119655	119758	-	4	4b

OE_24	AAACTGGCAAGGAGAGAAAA	GTTTTAGTGAGCCGAGACAGC	302	NW_018942 3.1	11596853	11596955	+	4	
OE_27	GTCCTTCAAAGGCTCACAGAT	TAGTTGAGTACACTGTTCCAGGAT	229	NW_016286 9.1	5365402	5365504	-	4a	
OE_28	GAGAAACATGAGGGTTTTGG	GATCAGAAGAGGCTGGATCTG	361	NW_016315 8.1	19298	19400	+	4a	
OE_31_v2	CAGCCTCACCGACAAACTTAG	TGGTGGTGGTGTGTAATCTCA	576	NW_016509 1.1	556436	556538	+	4a	
OE_32	TTCAAGCTGGGACTGCTCA	AGGAGGTTTCCAAGTCACAGA	287	NW_016575 7.1	4482954	4483060	-	4a	
OE_38	GGAGTCGGCCCATATTAAAAG	GCGCTCAAAGGTTCATTTTC	554	NW_017853 5.1	1006791	1006893	+	4a	
OE_39	CTGGCACAGACCTAAACAAAG	GGGTACTCTTCCAGTGCTCA	300	NW_017875 7.1	4217025	4217127	+	4a	
OE_41	GGCATTGTTTGGGTGTTACTG	CCCTTGTGCTAGATGAAGCTG	733	NW_018253 5.1	1154011	1154113	-	4a	
OE_43	GGCAAAAGCAGAAGAGTCAA	GGGAGCTCTACTTTTGGTTC	840	NW_018386 9.1	5673654	5673751	-	4a	
OE_45	GAAAACAACAAAATGGCAGGA	TTTGTTCCATACCTATTTCCATTC	331	NW_018448 0.1	863884	863986	-	4a	
OE_50	AGAAAGGCCCTCTGCATTTA	CCAGGCTACCAATGAAACAT	300	NW_018520 2.1	862626	862727	-	4a	
OE_51	TGGCACAATAGTGTGTCTTAACTG	TGTGACACTCATTTAGGCCTTT	811	NW_018542 4.1	2354464	2354566	-	4a	
OE_53	GGGAGAAGAAGAATCTGGTTGA	TGACACTGGTATCTGGAGCTG	301	NW_018653 5.1	5683168	5683260	+	4a	
OE_55	CCTTGGCAAAAGCCTGTTAGT	CAGGTGAAACAGAACCTCAACA	475	NW_018675 7.1	1875049	1875151	+	4a	
OE_58	AACACATGTTTATGGCCCAAT	CAGGAAAACCCAGCTACCATT	799	NW_018809 0.1	6532176	6532269	-	4a	
OE_62	TCCTGACCTCAAGTGATCTGC	TAGCTGTGTGAGAGAACCCAT	850	NW_019120 1.1	4096422	4096524	-	4a	
U_OM_90534	AAGCTGGGCCTTCCTAGTCT	ATTCAGGGCATTGTGGTACAG	290	NW_019053 4.1	959594	959696	+	4	4b
U_OM_73758_v2	GCACGAGGAATATCTCTTTGAA	TCTTTCCACCCTAATCTCACC	381	NW_017375 8.1	3202752	3202854	+	4a	

U_OM_91090_v2	ATGGTGCTACCCTCAAGTTCA	CTCACGTCAACTCTCAGATGAA	368	NW_012191090.1	7220727	7220829	-	4a	
U_OM_68979_v2	CAGCAAAAAGAGACAAGGAAAC	TGCACACTCAAAGCTCTCTTC	461	NW_012168979.1	8062006	8062108	-	4a	
U_OM_65535	AAGCAGAGGGCATTGAGC	CTGGACTTTCTACCTTCCCTAAT	569	NW_012165535.1	11528217	11528319	-	4a	
U_OM_85757	ACTCTTGGTACCCCAACACAA	ACTCCAACCTGGATGACAGAG	709	NW_012185757.1	11543495	11543596	-	4a	
U_OM_83869_v2	CCCCCTTTGTGTACATACTGC	GGCTGTTCATGAAGTAGCAGTC	389	NW_012183869.1	13603007	13603109	-	4a	
U_OM_89423_v3	AAGCCCAGTGGACATAAAAGA	CAAGGTGAGATGCCTTCTAGG	511	NW_012189423.1	18256638	18256738	-	4	4b
U_OM_89423_v4	CTTCCTGAACTCCATGTTTCC	TCTCCTGAACTATGCCTCACA	509	NW_012189423.1	18872686	18872789	-	3	4b
U_OM_63535_v2	GCATGCAACACACAGGAAAG	TTCTCAGCAGCTTGAATAGGC	342	NW_012163535.1	23826465	23826567	+	4a	
U_OM_89423_v5	GATTGAGTGACACCAACCAAA	AAATCAGTGCAACAGGGAGAA	489	NW_012189423.1	26061712	26061814	+	4a	
OE_29	CGCACATCTACAACCAACTGA	GCCAAGGCTGATGTTTACAAG	691	NW_012164202.1	2548324	2548426	+	4a	
U_OM_85425	TGTCAGAGCCTTTACCTGGAC	CCTCCTTTACATACACCCACA	547	NW_012185425.1	757056	757156	-	4a	

Table A2.4 Shared capuchin monkey and squirrel monkey primers

Locus	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')	Filled (bp)	Scaffold	Start	End	Strand	Platy-1 Subfamily
Ceb_3	CCTGTGCCTGACACATAGTAG	GGGAGAACATGACCTAAGCAG	270	NW_016107934.1	5844056	5844157	+	4a
U_Ceb_Platy1-4a_18	TTTTATATATCATTGTTCTGGGTTCC	GCAGCATTCCAAGTTCAAGA	285	NW_016107342.1	5041685	5041786	+	4a
217	CCACACTAGAAACCAGGGAAG	TCAGGGGAAAATCCCTGAG	373	NW_016107444.1	4085325	4085427	+	4a
Ply4a-7	CCTCTCTCCTCCCTTTCCAA	GCAGCATTCCAAGTTCAAGA	366	JH378200.1	8332658	8332761	+	4a
Ply4a-12	CCCTGAGCACTTAAATTAGCC	GGGAGAACATGACCTAAGCAG	360	JH378113.1	6462952	6463050	+	4a

Table A2.5 NWM DNA panel

Species	Common name	Origin	ID
Homo sapiens	Human	ATCC	HeLa CCL-2
Pan troglodytes	Common Chimpanzee	IPBIR	NS06006
Chlorocebus aethiops	African Green monkey	ATCC	CCL70
Lagothrix lagotricha	Woolly monkey	Coriell	NG05356
Ateles belzebuth	White bellied spider monkey	SDFZ	KB6701
Ateles geoffroyi	Blacked-handed spider monkey	Coriell	NG 05352
Alouatta sara	Bolivian red howler monkey	SDFZ	OR749
Callithrix jacchus	Common marmoset	NERPRC	cj393-99, A-2-738
Callithrix pygmea	Pygmy marmoset	SDFZ	OR690
Callimico goeldii	Goeldi's marmoset	Alan Harris	955
Saguinus labiatus	Red-chested mustached tamarin	Coriell	NG05308
Saguinus fuscicollis nigrifrons	Geoffroys saddle-back tamarin	SDFZ	OR621
Sapajus apella	Capuchin monkey	KP	CA003
Sapajus apella	Capuchin monkey	KP	30156
Sapajus apella	Capuchin monkey	KP	30157
Saimiri s. sciureus	Squirrel monkey	SDFZ	KB4544
Aotus trivirgatus	Owl monkey	ATCC	CRL1556
Pithecia p. pithecia	Norhtern white-faced saki	SDFZ	OR842
Callicebus d. donacophilus	Bolivian gray titi	SDFZ	OR1522

ATCC: From cell lines provided by the American Type Culture Collection
IPBIR: Integrated Primate Biomaterials and Information Resource
Coriell: Coriell Institute for Medical Research, 302 Haddon Avenue, Camden, NJ
SDFZ: San Diego Frozen Zoo, Conservation and Research for Endangered Species (CRES)
NERPRC: New England Regional Primate Research Center
KP: Kimberly Phillips, Trinity University

Table A2.6: Capuchin monkey DNA panel

Species	**Common name**	**Origin**	**ID**
Homo sapiens	Human	ATCC	Hela CCL-2
Callithrix jacchus	Common marmoset	NERPRC	cj393-99, A02-738
Saimiri s. sciureus	Common Squirrel monkey	SDFZ	KB4544
Aotus trivirgatus	Three-striped Owl monkey	ATCC	CRL1556
Cebus imitator	White-faced sapajou (Ref) (untufted)	Wash U.	Cc_AM_T3
Cebus capucinus	White-faced sapajou (untufted)	FMNH	UF 31995
Cebus capucinus	White-faced sapajou (untufted)	FMNH	UF 32380
Cebus albifrons	White-fronted capuchin monkey (untufted)	Chris C. Conroy	MVZ:Mamm:193675
Cebus albifrons	White-fronted capuchin monkey (untufted)	Chris C. Conroy	MVZ:Mamm:193676
Cebus albifrons albifrons	White-fronted capuchin monkey (untufted)	SDZICR	KB 4207
Sapajus appella	Tufted capuchin monkey	LSUMZ	LSUMZ M-6112
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46592
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46594
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46595
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46596
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46597
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46598
Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46599

ATCC: From cell lines provided by the American Type Culture Collection
NERPRC: New England Regional Primate Research Center
SDFZ: San Diego Frozen Zoo, Conservation and Research for Endangered Species (CRES)
FMNH: Florida Museum of Natural History Genetics Resources Repository
MVZ: Museum of Vertebrate Zoology, University of California, Berkeley
SDZICR: San Diego Zoo Global Biomaterials Review Group, San Diego Zoo Institute for Conservation Research
LSUMZ: LSU Museum of Natural Science Collection of Genetic Resources, 119 Foster Hall, Baton Rouge, LA
Wash U.: McDonnell Genome Institute-Washington University School of Medicine
UAM: University of Alaska Museum of the North Mammal Collection, Fairbanks, Alaska

Table A 2.7 Saimiri DNA panel

Species	Common name	Origin	ID
Homo sapiens	Human	ATCC	HeLa CCL-2
Callithrix jacchus	Common marmoset	NERPRC	cj393-99, A02-738
Saimiri s. sciureus	Common Squirrel monkey	SDFZ	KB4544
Saimiri sciureus	Common Squirrel monkey	LSUMZ	LSUMZ M-7827
Saimiri sciureus	Common Squirrel monkey	Burke	UWBM # 75531
Saimiri sciureus	Common Squirrel monkey	Burke	UWBM # 75532
Saimiri sciureus	Common Squirrel monkey	Coriell	NG05311
Saimiri sciureus	Common Squirrel monkey	Kristof Zyskowski	YPM MAM 015317
Saimiri sciureus	Common Squirrel monkey	Kristof Zyskowski	YPM MAM 015340
Saimiri sciureus	Common Squirrel monkey	Chris C. Conroy	MVZ Mamm 193661
Saimiri sciureus	Common Squirrel monkey	Chris C. Conroy	MVZ Mamm 193685
Saimiri sciureus	Common Squirrel monkey	KCCMR	6118
Saimiri sciureus	Common Squirrel monkey	KCCMR	658
Saimiri sciureus sciureus	Common Squirrel monkey	SDZICR	KB18803
Saimiri boliviensis	Bolivian squirrel monkey	LSUMZ	LSUMZ M-4970
Saimiri boliviensis	Bolivian squirrel monkey	Chris C. Conroy	MVZ Mamm 196088
Saimiri boliviensis	Bolivian squirrel monkey	John A. Vanchiere	H604 Liver DNA
Saimiri boliviensis	Bolivian squirrel monkey	John A. Vanchiere	H804 Liver DNA
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2212
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2514
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2240
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2427
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	4248
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2573
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2269
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2560
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2233
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	5161
Saimiri boliviensis peruviensis	Peruvian squirrel monkey	KCCMR	3526
Saimiri boliviensis peruviensis	Peruvian squirrel monkey	KCCMR	2291
Saimiri boliviensis peruviensis	Peruvian Black-Capped Squirrel Monkey	SDZICR	KB17911

Saimiri oerstedii oerstedii	Panamanian Red-Backed Squirrel Monkey	SDZICR	KB7456
Saimiri sciureus macrodon	Ecuadorian Squirrel Monkey	SDZICR	KB17915
Saimiri sp.	Squirrel Monkey	Chris C. Conroy	MVZ Mamm 196089

ATCC: From cell lines provided by the American Type Culture Collection
NERPRC: New England Regional Primate Research Center
SDFZ: San Diego Frozen Zoo, Conservation and Research for Endangered Species (CRES)
LSUMZ: LSU Museum of Natural Science Collection of Genetic Resources, 119 Foster Hall, Baton Rouge, LA
Burke: The Burke Museum of Natural HIstory and Culture, University of Washington, Seattle, WA
Coriell: Coriell Institute for Medical Research, 302 Haddon Avenue, Camden, NJ
YPM: Yale Peabody Museum of Natural History, Yale University, 170 Whitney Ave., New Haven, CT
MVZ: Museum of Vertebrate Zoology, University of California, Berkeley
JAV: John A. Vanchiere, M.D., Ph.D. Chief, Pediatric Infectious Diseases, LSUHSC-Shreveport, LA
KCCMR: Michael E. Keeling Center for Comparative Medicine and Research, The University of Texas MD Anderson Cancer Center, Bastrop, TX
SDZICR: San Diego Zoo Global Biomaterials Review Group, San Diego Zoo Institute for Conservation Research

Table A2.8 Aotus DNA panel

Species	Common name	Origin	ID	#
Homo sapiens	Human	ATCC	Hela CCL-2	1
Callithrix jacchus	Common marmoset	NERPRC	cj393-99, A02-738	2
Saimiri boliviensis	Bolivian squirrel monkey	KCCMR	2514	3
Aotus trivirgatus	Three-striped Owl Monkey	ATCC	CRL1556	4
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	85464	5
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	85676	6
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	86116	7
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	86334	8
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	85835	9
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	85974	10
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	86224	11
Aotus nancymaae	Nancy Ma's night monkey	SDZICR	KB9129	12
Aotus nancymaae	Nancy Ma's night monkey	KCCMR	85841	13
Aotus vociferans	Noisy owl monkey (Spix's night monkey)	Chris C. Conroy	MVZ Mamm 153465	14
Aotus vociferans	Noisy owl monkey (Spix's night monkey)	Chris C. Conroy	MVZ Mamm 155159	15
Aotus vociferans	Noisy owl monkey (Spix's night monkey)	KCCMR	86100	16
Aotus vociferans	Noisy owl monkey (Spix's night monkey)	KCCMR	86218	17
Aotus vociferans	Noisy owl monkey (Spix's night monkey)	KCCMR	85962	18
Aotus vociferans	Noisy owl monkey (Spix's night monkey)	KCCMR	86230	19
Aotus azarae	Azara's night monkey (southern night monkey)	KCCMR	85457	20
Aotus azarae	Azara's night monkey (southern night monkey)	KCCMR	85818	21
Aotus azarae	Azara's night monkey	SDZICR	KB10043	22
Aotus lemurinus griseimembra	Panamanian night monkey	SDZICR	KB4883	23
Aotus trivirgatus	Three-striped Owl Monkey	Museum Southwestern Biology	MSB:Mamm:212080	24
Aotus trivirgatus	Three-striped Owl Monkey	Museum Southwestern Biology	MSB:Mamm:41436	25
Aotus trivirgatus	Three-striped Owl Monkey	Museum Southwestern Biology	MSB:Mamm:56874	26

ATCC: From cell lines provided by the American Type Culture Collection
NERPRC: New England Regional Primate Research Center
KCCMR: Michael E. Keeling Center for Comparative Medicine and Research, The University of Texas MD Anderson Cancer Center, Bastrop, TX
SDZICR: San Diego Zoo Global Biomaterials Review Group, San Diego Zoo Institute for Conservation Research

MVZ: Museum of Vertebrate Zoology, University of California, Berkeley
MSB: Museum of Southwestern Biology, University of New Mexico

Table A2.9 Capuchin monkey PCR genotypes using the capuchin monkey DNA panel. " 0 0" indicates a homozygous absent band, "1 0" indicates a heterozygous insertion, and "1 1" indicates a homozygous present insertion.

#	CC_3		CC_5		CC_7		CC_8		UU_Ceb_1_Redo		UU_Ceb_2		UU_Ceb_4	
1	-9	-9	0	0	-9	-9	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	UU_Ceb_5		UU_Ceb_6		UU_Ceb_7		UU_Ceb_8		UU_Ceb_11		UU_Ceb_13_Redo		U_Ceb_Platy1-4_1	
1	0	0	0	0	-9	-9	-9	-9	0	0	-9	-9	-9	-9
2	0	0	0	0	0	0	0	0	0	0	-9	-9	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	-9	-9
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1

14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9

#	U_Ceb_Platy1-4a_21		U_Ceb_Platy1-5_23		U_Ceb_Platy1-4a_18		UU_Ceb_3		Ply4a-7		Ply4a-12		217	
1	-9	-9	-9	-9	-9	-9	0	0	0	0	0	0	-9	-9
2	0	0	0	0	0	0	0	0	0	0	0	0	-9	-9
3	-9	-9	0	0	1	1	1	1	1	1	1	1	1	1
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	-9	-9	1	1	1	1	1	1	-9	-9	1	1	1	1
8	1	1	1	1	1	1	1	1	-9	-9	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	-9	-9	1	1	1	1

Table A2.9 Key

#	Species	Common name	Origin	ID
1	*Homo sapiens*	Human	ATCC	Hela CCL-2
2	*Callithrix jacchus*	Common marmoset	NERPRC	cj393-99, A02-738
3	*Saimiri s. sciureus*	Common Squirrel monkey	SDFZ	KB4544
4	*Aotus trivirgatus*	Three-striped Owl monkey	ATCC	CRL1556
5	*Cebus imitator*	White-faced sapajou (Ref) (untufted)	Wash U.	Cc_AM_T3
6	*Cebus capucinus*	White-faced sapajou (untufted)	FMNH	UF 31995
7	*Cebus capucinus*	White-faced sapajou (untufted)	FMNH	UF 32380
8	*Cebus albifrons*	White-fronted capuchin monkey (untufted)	Chris C. Conroy	MVZ:Mamm:193675
9	*Cebus albifrons*	White-fronted capuchin monkey (untufted)	Chris C. Conroy	MVZ:Mamm:193676
10	*Cebus albifrons albifrons*	White-fronted capuchin monkey (untufted)	SDZICR	KB 4207

11	*Cebus (Sapajus) appella*	Tufted capuchin monkey	LSUMZ	LSUMZ M-6112
12	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46592
13	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46594
14	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46595
15	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46596
16	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46597
17	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46598
18	*Cebus (Sapajus) appella*	Tufted capuchin monkey	Dr. Link Olson	UAM 46599

Table A2.10 Saimri monkey PCR genotypes using the Saimiri DNA panel. " 0 0" indicates a homozygous absent band, "1 0" indicates a heterozygous insertion, and "1 1" indicates a homozygous present insertion.

#	Ply4a-8		Ply4a-10		Ply4a-12		Ply4a-16		Ply4a-17		Ply4a-21		Ply4a-25	
1	0	0	-9	-9	0	0	0	0	-9	-9	0	0	-9	-9
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	1	1	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1

25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1
27	1	1	1	1	1	1	1	1	1	1	1	1	1	1
28	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1	1	1	1	1	1	1
30	1	1	1	1	1	1	1	1	1	1	1	1	1	1
31	1	1	1	1	1	1	1	1	1	1	1	1	1	1
32	1	1	1	1	1	1	1	1	1	1	1	1	1	1
33	1	1	1	1	1	1	1	1	1	1	1	1	1	1
34	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	Ply4a-27		Ply4a-30		Ply4a-34		Ply4a-37		Ply4a-46		Ply4-1		Ply5-12	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	1	1	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1
27	1	1	1	1	1	1	1	1	1	1	1	1	1	1
28	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1	1	1	1	1	1	1

30	1	1	1	1	1	1	1	1	1	1	1	1	1	1
31	1	1	1	1	1	1	1	1	1	1	1	1	1	1
32	1	1	1	1	1	1	1	1	1	1	1	1	1	1
33	1	1	1	1	1	1	1	1	1	1	1	1	1	1
34	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	E_30		E_31		E_32		E_38		E_43		E_45		Ply4a-7	
1	-9	-9	-9	-9	0	0	-9	-9	0	0	-9	-9	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	1	1	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1
27	1	1	1	1	1	1	1	1	1	1	1	1	1	1
28	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1	1	1	1	1	1	1
30	1	1	1	1	1	1	1	1	1	1	1	1	1	1
31	1	1	1	1	1	1	1	1	1	1	1	1	1	1
32	1	1	1	1	1	1	1	1	1	1	1	1	1	1
33	1	1	1	1	1	1	1	1	1	1	1	1	1	1
34	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	Ply4a-12		UU_Ceb_3		217		U_Ceb_Platy1-4a_18	
1	0	0	0	0	-9	-9	0	0
2	0	0	0	0	-9	-9	0	0
3	1	1	1	1	1	1	1	1
4	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1
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23	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1
27	1	1	1	1	1	1	1	1
28	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1
30	1	1	1	1	1	1	1	1
31	1	1	1	1	1	1	1	1
32	1	1	1	1	1	1	1	1
33	1	1	1	1	1	1	1	1
34	1	1	1	1	1	1	1	1

Table 2.10 Key

#	Species	Common name	Origin	ID
1	*Homo sapiens*	Human	ATCC	HeLa CCL-2
2	*Callithrix jacchus*	Common marmoset	NERPRC	cj393-99, A02-738
3	*Saimiri s. sciureus*	Common Squirrel monkey	SDFZ	KB4544
4	*Saimiri sciureus*	Common Squirrel monkey	LSUMZ	LSUMZ M-7827
5	*Saimiri sciureus*	Common Squirrel monkey	Burke	UWBM # 75531
6	*Saimiri sciureus*	Common Squirrel monkey	Burke	UWBM # 75532
7	*Saimiri sciureus*	Common Squirrel monkey	Coriell	NG05311
8	*Saimiri sciureus*	Common Squirrel monkey	Kristof Zyskowski	YPM MAM 015317
9	*Saimiri sciureus*	Common Squirrel monkey	Kristof Zyskowski	YPM MAM 015340
10	*Saimiri sciureus*	Common Squirrel monkey	Chris C. Conroy	MVZ Mamm 193661
11	*Saimiri sciureus*	Common Squirrel monkey	Chris C. Conroy	MVZ Mamm 193685
12	*Saimiri sciureus*	Common Squirrel monkey	KCCMR	6118
13	*Saimiri sciureus*	Common Squirrel monkey	KCCMR	658
14	*Saimiri sciureus sciureus*	Common Squirrel monkey	SDZICR	KB18803
15	*Saimiri boliviensis*	Bolivian squirrel monkey	LSUMZ	LSUMZ M-4970
16	*Saimiri boliviensis*	Bolivian squirrel monkey	Chris C. Conroy	MVZ Mamm 196088
17	*Saimiri boliviensis*	Bolivian squirrel monkey	John A. Vanchiere	H604 Liver DNA
18	*Saimiri boliviensis*	Bolivian squirrel monkey	John A. Vanchiere	H804 Liver DNA
19	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2212
20	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2514
21	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2240
22	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2427
23	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	4248
24	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2573
25	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2269
26	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2560
27	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2233
28	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	5161
29	*Saimiri boliviensis peruviensis*	Peruvian squirrel monkey	KCCMR	3526

30	*Saimiri boliviensis peruviensis*	Peruvian squirrel monkey	KCCMR	2291
31	*Saimiri boliviensis peruviensis*	Peruvian Black-Capped Squirrel Monkey	SDZICR	KB17911
32	*Saimiri oerstedii oerstedii*	Panamanian Red-Backed Squirrel Monkey	SDZICR	KB7456
33	*Saimiri sciureus macrodon*	Ecuadorian Squirrel Monkey	SDZICR	KB17915
34	*Saimiri sp.*	Squirrel Monkey	Chris C. Conroy	MVZ Mamm 196089

Table A2.11 Aotus monkey PCR genotype using the aotus monkey DNA panel. " 0 0" indicates a homozygous absent band, "1 0" indicates a heterozygous insertion, and "1 1" indicates a homozygous present insertion.

#	U_OM_72535		U_OM_87201		U_OM_87757		U_OM_67868		U_OM_69313		U_OM_90080		U_OM_73758	
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2	0	0	0	0	0	0	0	0	-9	-9	0	0	0	0
3	0	0	0	0	0	0	0	0	-9	-9	0	0	0	0
4	0	0	0	0	1	1	1	1	1	1	1	1	1	1
5	0	0	1	1	1	1	1	1	1	1	1	1	1	1
6	1	0	1	1	1	1	1	1	1	1	1	1	1	1
7	0	0	1	1	1	1	1	1	1	1	1	1	1	1
8	1	0	1	1	1	1	1	1	1	1	1	1	1	1
9	1	0	1	1	1	1	1	1	1	1	1	1	1	1
10	1	0	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	0	0	1	1	1	1	1	1	1	1	1	1	1	1
13	0	0	1	1	1	1	1	1	1	1	1	1	1	1
14	0	0	0	0	1	1	1	1	1	1	1	1	1	1
15	0	0	0	0	1	1	1	1	1	1	1	1	1	1
16	0	0	0	0	1	1	1	1	1	1	1	1	1	1
17	0	0	0	0	1	1	1	1	1	1	1	1	1	1
18	0	0	0	0	1	1	1	1	1	1	1	1	1	1
19	0	0	0	0	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	0	0	0	0	1	0	1	1	1	1	-9	-9	1	1
24	0	0	0	0	1	1	1	1	1	1	1	1	1	1
25	0	0	0	0	1	1	1	1	1	1	1	1	1	1
26	0	0	0	0	1	1	1	1	1	1	1	1	1	1

#	U_OM_79090		U_OM_80979		U_OM_73201		U_OM_83869		U_OM_85757_v2		U_OM_84269		U_OM_71126	
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3	0	0	0	0	0	0	0	0	-9	-9	0	1	0	0
4	-9	-9	1	1	1	1	0	0	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	-9	-9	1	1	1	1	1	1
23	1	1	1	1	1	1	0	0	1	1	1	0	0	0
24	1	1	1	1	1	1	0	0	1	1	1	1	1	1
25	1	1	1	1	1	1	0	0	1	1	1	1	1	1
26	1	1	1	1	1	1	0	0	1	1	1	1	1	1

#	U_OM_71201		U_OM_85913		U_OM_79424		U_OM_86114		U_OM_76313		U_OM_84436		U_OM_81312	
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3	0	0	0	0	0	0	-9	-9	0	0	0	0	0	0
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	-9	-9	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1

12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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21	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
22	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
23	1	1	1	1	1	1	1	1	1	1	1	0	1	1
24	1	1	1	1	1	1	-9	-9	1	1	1	1	1	1
25	1	1	1	1	1	1	-9	-9	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_84513		U_OM_83802		U_OM_89423		U_OM_81868		U_OM_83813		U_OM_85957		U_OM_89979	
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3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	0	1	1	1	1	1	1	0	0	1	0	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1

25	1	1	1	1	1	1	1	1	-9	-9	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_73423		U_OM_85458		U_OM_66202		U_OM_89201		U_OM_76646		U_OM_78901		U_OM_85202	
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3	0	0	-9	-9	0	0	0	0	0	0	0	0	0	0
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6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	-9	-9	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	0	1	1	1	1	1	0	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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#	U_OM_76757		U_OM_91312		U_OM_64424		U_OM_67424		U_OM_84424		U_OM_73536		U_OM_84147	
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3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9

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11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	-9	-9	1	1	1	1
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21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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24	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
25	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
26	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_68646		U_OM_85646		U_OM_91090		U_OM_68313		U_OM_80424		U_OM_67202		U_OM_62647	
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3	-9	-9	-9	-9	0	0	0	0	0	0	0	0	0	0
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6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
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21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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23	1	1	1	1	1	1	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_91423		U_OM_71312		U_OM_84868		U_OM_86091		U_OM_91201		U_OM_62869		U_OM_74202	
1	-9	-9	0	0	0	0	0	0	-9	-9	-9	-9	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1

6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
10	1	1	-9	-9	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	-9	-9	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	0	0	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_88312		U_OM_64646		U_OM_86535		U_OM_84313		U_OM_87313		U_OM_85313		U_OM_82423	
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2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	-9	-9	0	0	0	0	0	0
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1

19	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
20	0	0	1	1	1	1	1	1	1	1	1	1	1	1
21	0	0	1	1	1	1	1	1	1	1	1	1	1	1
22	0	0	1	1	1	1	1	1	1	1	1	1	-9	-9
23	1	1	1	0	1	1	1	1	1	1	-9	-9	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_74646		U_OM_86901_v2		U_OM_66868		U_OM_90534_v2		U_OM_72423		U_OM_85657		U_OM_73534	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	-9	-9	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	1	1	1	1	1	0	1	1	1	0
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	OE_2		OE_3		OE_6		OE_7		OE_8		OE_9		OE_10_v2	
1	-9	-9	-9	-9	-9	-9	-9	-9	0	0	0	0	-9	-9
2	-9	-9	-9	-9	0	0	0	0	0	0	0	0	0	0
3	-9	-9	-9	-9	0	0	-9	-9	0	0	0	0	0	0

4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	0	0	1	1	1	1	1	1
15	1	1	1	1	1	1	0	0	1	1	1	1	1	1
16	1	1	1	1	1	1	0	0	1	1	1	1	1	1
17	1	1	1	1	1	1	0	0	1	1	1	1	1	1
18	1	1	1	1	1	1	0	0	1	1	1	1	1	1
19	1	1	1	1	1	1	0	0	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
23	-9	-9	1	1	1	0	1	1	1	1	1	0	1	0
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	OE_11		OE_13_V2		OE_16		OE_19		OE_22		OE_23		OE_24	
1	-9	-9	-9	-9	-9	-9	-9	-9	-9	-9	0	0	0	0
2	-9	-9	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	-9	-9	-9	-9	0	0	0	0	0	0	0	0
4	1	1	1	1	0	0	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	0
7	1	1	1	1	1	0	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	0	1	1	1	1	1	1	1	1

17	1	1	1	1	0	0	1	1	1	1	1	1	1	1
18	1	1	1	1	1	0	1	1	1	1	1	1	1	1
19	1	1	1	1	1	0	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	0	0	1	1	1	1	1	0	1	1
24	1	1	1	1	0	0	1	1	1	1	1	1	1	1
25	1	1	1	1	0	0	1	1	1	1	1	1	1	1
26	1	1	1	1	0	0	1	1	1	1	1	1	1	1

#	OE_27		OE_28		OE_31_v2		OE_32		OE_38		OE_39		OE_41	
1	-9	-9	0	0	-9	-9	0	0	0	0	-9	-9	0	0
2	0	0	-9	-9	0	0	0	0	0	0	0	0	0	0
3	-9	-9	-9	-9	-9	-9	0	0	-9	-9	0	0	0	0
4	1	1	0	0	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23	1	1	1	1	1	1	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	OE_43		OE_45		OE_50		OE_51		OE_53		OE_55		OE_58	
1	-9	-9	-9	-9	0	0	-9	-9	0	0	-9	-9	-9	-9

2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	-9	-9	-9	-9
4	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	-9	-9	1	1	1	1	1	1	1	1	1	1	1	1
23	0	0	1	1	1	1	1	1	1	0	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	OE_62		U_OM_90534		U_OM_73758_v2		U_OM_91090_v2		U_OM_68979_v2		U_OM_65535		U_OM_85757	
1	-9	-9	0	0	0	0	-9	-9	0	0	-9	-9	-9	-9
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	-9	-9	0	0	0	0	0	0	0	0	0	0	-9	-9
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9
13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1

15	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9
23	1	1	1	1	1	1	1	1	1	0	1	1	1	1
24	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1

#	U_OM_83869_v2		U_OM_89423_v3		U_OM_89423_v4		U_OM_63535_v2		U_OM_89423_v5		OE_29		U_OM_85425	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	-9	-9	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	-9	-9	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	1	1	1	1	-9	-9	1	1	1	1	1	1	1	1
13	1	1	1	1	-9	-9	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	0	1	1	1	1
15	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	-9	-9	1	1	1	1	1	1	1	1
23	1	1	1	1	-9	-9	1	1	1	1	1	1	1	0
24	1	1	1	1	1	1	1	1	1	1	1	1	1	0
25	1	1	1	1	1	1	1	1	1	1	1	1	1	0
26	1	1	1	1	1	1	1	1	1	1	1	1	1	0

Table A2.11 Key

#	Species	Common name	Origin	ID
1	*Homo sapiens*	Human	ATCC	HeLa CCL-2
2	*Callithrix jacchus*	Common marmoset	NERPC	cj393-99, A02-738
3	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2514
4	*Aotus trivirgatus*	Three-srtiped owl monkey	ATCC	CRL1556
5	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85464
6	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85676
7	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	86116
8	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	86334
9	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85835
10	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85974
11	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	86224
12	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	KB9129
13	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85841
14	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	Chris C. Conroy	MVZ Mamm 153465
15	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	Chris C. Conroy	MVZ Mamm 155159
16	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	86100
17	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	86218
18	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	85962
19	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	86230
20	*Aotus azarae*	Azara's night monkey (southern night monkey)	KCCMR	85457
21	*Aotus azarae*	Azara's night monkey (southern night monkey)	KCCMR	85818
22	*Aotus azarae*	Azara's night monkey	SDZICR	KB10043
23	*Aotus lemurinus griseimembra*	Panamanian night monkey	SDZICR	KB4883
24	*Aotus trivirgatus*	Three-striped owl monkey	Museum Southwestern Biology	MSB:Mamm:212080
25	*Aotus trivirgatus*	Three-striped owl monkey	Museum Southwestern Biology	MSB:Mamm:41436
26	*Aotus trivirgatus*	Three-striped owl monkey	Museum Southwestern Biology	MSB:Mamm:56874

Table A2.12 Capuchin monkey Platy-1 element divergence. Green highlight indicates a predicted lineage-specific insertion; yellow highlight indicates a predicated lineage-specific insertion that was PCR-analyzed.

Locus	% divergence	Percent	Age (my)
Cebus_Platy-1-1_NW_016107606.1_1100449-1100543_+	8.5	0.085	14.11023
Cebus_Platy-1-1_NW_016107397.1_80237-80339_-	8.8	0.088	14.60823
Cebus_Platy-1-1_NW_016107441.1_3980371-3980473_-	8.8	0.088	14.60823
Cebus_Platy-1-1_NW_016107416.1_2929272-2929374_-	9.9	0.099	16.43426
Cebus_Platy-1-1_NW_016107351.1_5822033-5822136_+	9.9	0.099	16.43426
Cebus_Platy-1-1_NW_016107348.1_3993708-3993811_+	10.2	0.102	16.93227
Cebus_Platy-1-1_NW_016107394.1_2692373-2692470_+	10.4	0.104	17.26428
Cebus_Platy-1-1_NW_016107593.1_2713183-2713285_-	10.8	0.108	17.92829
Cebus_Platy-1-1_NW_016107339.1_5388965-5389066_+	10.9	0.109	18.09429
Cebus_Platy-1-1_NW_016107357.1_15660334-15660436_+	10.9	0.109	18.09429
Cebus_Platy-1-1_NW_016107339.1_12242931-12243025_-	11.7	0.117	19.42231
Cebus_Platy-1-1_NW_016107658.1_791138-791239_+	11.9	0.119	19.75432
Cebus_Platy-1-1_NW_016107535.1_1957444-1957550_+	12	0.12	19.92032
Cebus_Platy-1-1_NW_016107372.1_1592298-1592400_+	12.4	0.124	20.58433
Cebus_Platy-1-1_NW_016107596.1_2704565-2704673_+	13	0.13	21.58035
Cebus_Platy-1-1_NW_016107931.1_283694-283797_-	13.9	0.139	23.07437
Cebus_Platy-1-1_NW_016107528.1_1082269-1082370_-	14	0.14	23.24037
Cebus_Platy-1-1_NW_016107357.1_18141251-18141354_+	14.6	0.146	24.23639
Cebus_Platy-1-1_NW_016107387.1_4889096-4889198_-	14.8	0.148	24.56839
Cebus_Platy-1-1_NW_016107394.1_3898414-3898510_+	15.6	0.156	25.89641
Cebus_Platy-1-1_NW_016107626.1_2670867-2670967_+	16	0.16	26.56042
Cebus_Platy-1-1_NW_016107347.1_10185112-10185208_-	16.8	0.168	27.88845
Cebus_Platy-1-1_NW_016107993.1_545299-545402_-	17.5	0.175	29.05046
Cebus_Platy-1-1_NW_016107424.1_436525-436627_+	17.5	0.175	29.05046
Cebus_Platy-1-1_NW_016107484.1_1478783-1478885_-	17.6	0.176	29.21647
Cebus_Platy-1-1_NW_016107549.1_1554025-1554128_-	23.7	0.237	39.34263
Cebus_Platy-1-2_NW_016107358.1_7808976-7809060_-	7.1	0.071	11.78619
Cebus_Platy-1-2_NW_016107760.1_372388-372490_-	7.8	0.078	12.94821
Cebus_Platy-1-2_NW_016107403.1_1281490-1281592_+	7.8	0.078	12.94821
Cebus_Platy-1-2_NW_016108138.1_188481-188578_+	8.3	0.083	13.77822
Cebus_Platy-1-2_NW_016107672.1_2221977-2222079_+	8.8	0.088	14.60823
Cebus_Platy-1-2_NW_016107915.1_683681-683783_+	9.8	0.098	16.26826
Cebus_Platy-1-2_NW_016108044.1_763160-763263_+	10.7	0.107	17.76228
Cebus_Platy-1-2_NW_016107348.1_892399-892500_-	11.9	0.119	19.75432
Cebus_Platy-1-2_NW_016107415.1_6115959-6116060_-	12.2	0.122	20.25232
Cebus_Platy-1-2_NW_016107482.1_3179792-3179894_-	13	0.13	21.58035
Cebus_Platy-1-2_NW_016107629.1_1918019-1918120_-	13.7	0.137	22.74236

Cebus_Platy-1-2_NW_016107471.1_811140-811242_-	14.7	0.147	24.40239
Cebus_Platy-1-2_NW_016107326.1_10270754-10270855_+	15.2	0.152	25.2324
Cebus_Platy-1-2_NW_016107397.1_780662-780762_+	16.2	0.162	26.89243
Cebus_Platy-1-2_NW_016107402.1_4213001-4213102_+	18.8	0.188	31.2085
Cebus_Platy-1-2_NW_016107443.1_2705990-2706087_-	8.2	0.082	13.61222
Cebus_Platy-1-2a_NW_016107402.1_2539667-2539764_+	4.1	0.041	6.806109
Cebus_Platy-1-2a_NW_016107402.1_2539663-2539763_+	4.1	0.041	6.806109
Cebus_Platy-1-2a_NW_016107333.1_9841584-9841687_+	4.8	0.048	7.968127
Cebus_Platy-1-2a_NW_016107700.1_416956-417059_+	5	0.05	8.300133
Cebus_Platy-1-2a_NW_016107983.1_156513-156615_+	6.2	0.062	10.29216
Cebus_Platy-1-2a_NW_016107936.1_307451-307549_+	6.4	0.064	10.62417
Cebus_Platy-1-2a_NW_016107604.1_2428361-2428463_-	6.9	0.069	11.45418
Cebus_Platy-1-2a_NW_016107362.1_2615145-2615247_+	6.9	0.069	11.45418
Cebus_Platy-1-2a_NW_016107934.1_161041-161143_-	7	0.07	11.62019
Cebus_Platy-1-2a_NW_016107383.1_6412390-6412491_+	7.1	0.071	11.78619
Cebus_Platy-1-2a_NW_016107784.1_408113-408205_-	7.6	0.076	12.6162
Cebus_Platy-1-2a_NW_016107575.1_1861512-1861614_-	7.8	0.078	12.94821
Cebus_Platy-1-2a_NW_016107700.1_463831-463934_-	7.8	0.078	12.94821
Cebus_Platy-1-2a_NW_016107349.1_4580724-4580826_-	7.8	0.078	12.94821
Cebus_Platy-1-2a_NW_016107351.1_4607530-4607631_-	8	0.08	13.28021
Cebus_Platy-1-2a_NW_016107417.1_3119322-3119424_+	8	0.08	13.28021
Cebus_Platy-1-2a_NW_016107633.1_517718-517819_+	8	0.08	13.28021
Cebus_Platy-1-2a_NW_016107354.1_2689500-2689590_+	8	0.08	13.28021
Cebus_Platy-1-2a_NW_016107391.1_699610-699710_+	9	0.09	14.94024
Cebus_Platy-1-2a_NW_016107446.1_4514009-4514111_+	9.8	0.098	16.26826
Cebus_Platy-1-2a_NW_016107375.1_9245083-9245185_+	9.9	0.099	16.43426
Cebus_Platy-1-2a_NW_016107574.1_995809-995911_+	10.2	0.102	16.93227
Cebus_Platy-1-2a_NW_016107380.1_1798302-1798405_-	10.7	0.107	17.76228
Cebus_Platy-1-2a_NW_016107667.1_1318076-1318178_-	10.8	0.108	17.92829
Cebus_Platy-1-2a_NW_016107453.1_748630-748732_+	11	0.11	18.26029
Cebus_Platy-1-2a_NW_016107390.1_847836-847938_+	11.1	0.111	18.42629
Cebus_Platy-1-2a_NW_016107595.1_2835819-2835916_+	11.3	0.113	18.7583
Cebus_Platy-1-2a_NW_016107481.1_2160608-2160708_+	11.3	0.113	18.7583
Cebus_Platy-1-2a_NW_016107353.1_945113-945212_+_former_2	13.1	0.131	21.74635
Cebus_Platy-1-2a_NW_016108172.1_4178-4280_-	13.9	0.139	23.07437
Cebus_Platy-1-2a_NW_016107333.1_9388012-9388113_+	14	0.14	23.24037
Cebus_Platy-1-2a_NW_016107514.1_1090224-1090325_-	14.1	0.141	23.40637
Cebus_Platy-1-2a_NW_016107678.1_1104652-1104751_+	15.2	0.152	25.2324
Cebus_Platy-1-2a_NW_016107379.1_4937622-4937720_+	15.3	0.153	25.39841
Cebus_Platy-1-2a_NW_016107692.1_1720268-1720372_-	16.4	0.164	27.22444
Cebus_Platy-1-2a_NW_016107316.1_5669745-5669847_+	17.5	0.175	29.05046

Cebus_Platy-1-2b_NW_016107391.1_577350-577441_+	5.6	0.056	9.296149
Cebus_Platy-1-2b_NW_016107328.1_8022270-8022372_+	6.2	0.062	10.29216
Cebus_Platy-1-2b_NW_016107742.1_391991-392092_-	7	0.07	11.62019
Cebus_Platy-1-2b_NW_016107377.1_595564-595666_-	7.8	0.078	12.94821
Cebus_Platy-1-2b_NW_016107337.1_5974884-5974986_+	7.8	0.078	12.94821
Cebus_Platy-1-2b_NW_016107702.1_1253551-1253652_+	7.9	0.079	13.11421
Cebus_Platy-1-2b_NW_016107581.1_1721138-1721241_+	9.1	0.091	15.10624
Cebus_Platy-1-2b_NW_016107319.1_5359646-5359743_+	9.4	0.094	15.60425
Cebus_Platy-1-2b_NW_016107372.1_3718977-3719073_-	9.4	0.094	15.60425
Cebus_Platy-1-2b_NW_016107383.1_7993051-7993145_-	9.7	0.097	16.10226
Cebus_Platy-1-2b_NW_016107518.1_322793-322894_+	10.9	0.109	18.09429
Cebus_Platy-1-2b_NW_016107956.1_825775-825868_+	10.9	0.109	18.09429
Cebus_Platy-1-2b_NW_016107357.1_3385712-3385814_+	10.9	0.109	18.09429
Cebus_Platy-1-2b_NW_016107814.1_918128-918230_+	11.8	0.118	19.58831
Cebus_Platy-1-2b_NW_016107822.1_638497-638599_+	11.8	0.118	19.58831
Cebus_Platy-1-2b_NW_016107379.1_7954829-7954931_+	11.8	0.118	19.58831
Cebus_Platy-1-2b_NW_016107445.1_1627578-1627680_-	11.9	0.119	19.75432
Cebus_Platy-1-2b_NW_016107348.1_1289246-1289348_+	13.9	0.139	23.07437
Cebus_Platy-1-2b_NW_016107534.1_960620-960723_-	14.6	0.146	24.23639
Cebus_Platy-1-2b_NW_016107902.1_878816-878918_-	16.8	0.168	27.88845
Cebus_Platy-1-2b_NW_016107402.1_4212997-4213098_+_former_2	21.8	0.218	36.18858
Cebus_Platy-1-3_NW_016107342.1_3264885-3264986_+	4.2	0.042	6.972112
Cebus_Platy-1-3_NW_016107520.1_2937869-2937971_-	4.9	0.049	8.13413
Cebus_Platy-1-3_NW_016107390.1_3928458-3928543_-	5.6	0.056	9.296149
Cebus_Platy-1-3_NW_016107469.1_1704239-1704341_-	5.9	0.059	9.794157
Cebus_Platy-1-3_NW_016107327.1_11460725-11460826_-	5.9	0.059	9.794157
Cebus_Platy-1-3_NW_016107366.1_7666126-7666228_+	6.9	0.069	11.45418
Cebus_Platy-1-3_NW_016107351.1_1449572-1449666_-	7.6	0.076	12.6162
Cebus_Platy-1-3_NW_016107397.1_8328478-8328580_-	7.8	0.078	12.94821
Cebus_Platy-1-3_NW_016107391.1_2359210-2359312_+	8.2	0.082	13.61222
Cebus_Platy-1-3_NW_016108198.1_124159-124255_-	8.7	0.087	14.44223
Cebus_Platy-1-3_NW_016107973.1_234452-234555_+	9.7	0.097	16.10226
Cebus_Platy-1-3_NW_016107553.1_3070015-3070116_+	9.9	0.099	16.43426
Cebus_Platy-1-3_NW_016107317.1_6960708-6960808_+	10	0.1	16.60027
Cebus_Platy-1-3_NW_016107717.1_1756515-1756616_+	10.1	0.101	16.76627
Cebus_Platy-1-3_NW_016107552.1_1950140-1950241_+	10.8	0.108	17.92829
Cebus_Platy-1-3_NW_016107826.1_779554-779656_-	10.9	0.109	18.09429
Cebus_Platy-1-3_NW_016107835.1_1328201-1328303_+	11.2	0.112	18.5923
Cebus_Platy-1-3_NW_016107850.1_884787-884889_-	11.8	0.118	19.58831
Cebus_Platy-1-3_NW_016107357.1_14360638-14360743_-	11.8	0.118	19.58831
Cebus_Platy-1-3_NW_016107341.1_9438961-9439063_+	11.8	0.118	19.58831

Cebus_Platy-1-3_NW_016107793.1_1060781-1060883_+	12	0.12	19.92032
Cebus_Platy-1-3_NW_016107512.1_657003-657084_-	12.3	0.123	20.41833
Cebus_Platy-1-3_NW_016107327.1_11751171-11751273_-	13.7	0.137	22.74236
Cebus_Platy-1-3_NW_016107345.1_6725864-6725966_+	13.7	0.137	22.74236
Cebus_Platy-1-4_NW_016107418.1_3421589-3421691_+	14	0.14	23.24037
Cebus_Platy-1-4_NW_016107564.1_562265-562368_+	3.9	0.039	6.474104
Cebus_Platy-1-4a_NW_016107477.1_3282050-3282151_+	1	0.01	1.660027
Cebus_Platy-1-4a_NW_016107435.1_3016219-3016320_-	2	0.02	3.320053
Cebus_Platy-1-4a_NW_016107707.1_959430-959531_+	2	0.02	3.320053
Cebus_Platy-1-4a_NW_016107368.1_3139387-3139489_-	2.9	0.029	4.814077
Cebus_Platy-1-4a_NW_016107408.1_6305816-6305918_-	3	0.03	4.98008
Cebus_Platy-1-4a_NW_016107394.1_5844056-5844157_+	3	0.03	4.98008
Cebus_Platy-1-4a_NW_016107423.1_2912227-2913528_-	3	0.03	4.98008
Cebus_Platy-1-4a_NW_016107324.1_3565978-3566080_+	3.9	0.039	6.474104
Cebus_Platy-1-4a_NW_016107517.1_4159111-4159208_+	4.1	0.041	6.806109
Cebus_Platy-1-4a_NW_016107736.1_711960-712055_-	4.2	0.042	6.972112
Cebus_Platy-1-4a_NW_016107774.1_1415826-1415928_+	4.9	0.049	8.13413
Cebus_Platy-1-4a_NW_016107350.1_542274-542376_+	4.9	0.049	8.13413
Cebus_Platy-1-4a_NW_016107511.1_2631683-2631785_-	5	0.05	8.300133
Cebus_Platy-1-4a_NW_016108056.1_141474-141576_-	5	0.05	8.300133
Cebus_Platy-1-4a_NW_016107411.1_3019364-3019465_-	5	0.05	8.300133
Cebus_Platy-1-4a_NW_016107340.1_10634567-10634667_+	5	0.05	8.300133
Cebus_Platy-1-4a_NW_016107342.1_5041685-5041786_+	5	0.05	8.300133
Cebus_Platy-1-4a_NW_016107403.1_2828681-2828782_+	5.2	0.052	8.632138
Cebus_Platy-1-4a_NW_016107357.1_11428699-11428801_+	5.9	0.059	9.794157
Cebus_Platy-1-4a_NW_016107367.1_7992271-7993572_-	6.1	0.061	10.12616
Cebus_Platy-1-4a_NW_016107956.1_586937-587040_-	6.8	0.068	11.28818
Cebus_Platy-1-4a_NW_016107564.1_797100-797202_-	6.9	0.069	11.45418
Cebus_Platy-1-4a_NW_016107365.1_7945868-7945971_-	6.9	0.069	11.45418
Cebus_Platy-1-4a_NW_016107444.1_4085325-4085427_+	6.9	0.069	11.45418
Cebus_Platy-1-4a_NW_016107553.1_1843767-1843852_-	7.1	0.071	11.78619
Cebus_Platy-1-4a_NW_016107374.1_7094536-7094634_-	7.1	0.071	11.78619
Cebus_Platy-1-4a_NW_016107343.1_6515664-6515764_-	8.3	0.083	13.77822
Cebus_Platy-1-4a_NW_016107520.1_3286752-3286853_+	8.9	0.089	14.77424
Cebus_Platy-1-4a_NW_016107324.1_6877109-6877213_+	9	0.09	14.94024
Cebus_Platy-1-4a_NW_016107551.1_3412237-3412339_+	9.9	0.099	16.43426
Cebus_Platy-1-4a_NW_016107319.1_11900022-11901326_-	10.5	0.105	17.43028
Cebus_Platy-1-4a_NW_016107500.1_3905602-3906904_-	12.1	0.121	20.08632
Cebus_Platy-1-4a_NW_016107788.1_759882-759985_-	13	0.13	21.58035
Cebus_Platy-1-4a_NW_016107649.1_961901-963203_-	13.3	0.133	22.07835
Cebus_Platy-1-5_NW_016107792.1_131192-131297_-	4.8	0.048	7.968127

Cebus_Platy-1-5_NW_016108013.1_249145-249251_+	4.8	0.048	7.968127
Cebus_Platy-1-5_NW_016107831.1_219785-219890_+	5.8	0.058	9.628154
Cebus_Platy-1-5_NW_016107482.1_5012032-5012132_+	6	0.06	9.960159
Cebus_Platy-1-5_NW_016107350.1_9467094-9467196_-	6.9	0.069	11.45418
Cebus_Platy-1-5_NW_016107317.1_11811919-11812019_-	7	0.07	11.62019
Cebus_Platy-1-5_NW_016107519.1_3022845-3022952_-	8.4	0.084	13.94422
Cebus_Platy-1-5_NW_016107518.1_2956676-2956781_+	8.6	0.086	14.27623
Cebus_Platy-1-5_NW_016107952.1_705047-705154_+	11.2	0.112	18.5923
Cebus_Platy-1-5_NW_016108037.1_413787-413889_+	11.9	0.119	19.75432
Cebus_Platy-1-5_NW_016107425.1_5445313-5445413_+	13.1	0.131	21.74635
Cebus_Platy-1-6_NW_016107410.1_2738288-2738390_+	24.5	0.245	40.67065

Table A2.13 Squirrel monkey Platy-1 element divergence. Green highlight indicates a predicted lineage-specific insertion; yellow highlight indicates a predicated lineage-specific insertion that was PCR-analyzed.

Locus	% divergence	Percent	Age
Saimiri_Platy-1-1_NW_003943671.1_10037558:10040061_+	4.9	0.049	8.13413
Saimiri_Platy-1-1_NW_003943650.1_5633262:5635766_+	5	0.05	8.300133
Saimiri_Platy-1-1_NW_003943618.1_26058436:26060938_+	9.2	0.092	15.27224
Saimiri_Platy-1-1_NW_003943637.1_20490443:20492946_-	9.8	0.098	16.26826
Saimiri_Platy-1-1_NW_003943612.1_3334266:3336763_+	10.5	0.105	17.43028
Saimiri_Platy-1-1_NW_003943665.1_13868893:13871395_-	11.8	0.118	19.58831
Saimiri_Platy-1-1_NW_003943637.1_2884851:2887353_+	12	0.12	19.92032
Saimiri_Platy-1-1_NW_003943624.1_10111290:10113792_+	12.2	0.122	20.25232
Saimiri_Platy-1-1_NW_003943732.1_4276562:4279064_+	12.8	0.128	21.24834
Saimiri_Platy-1-1_NW_003943624.1_18711288:18713795_+	13	0.13	21.58035
Saimiri_Platy-1-1_NW_003943733.1_3711597:3714093_-	13.8	0.138	22.90837
Saimiri_Platy-1-1_NW_003943636.1_8777451:8779953_+	14.1	0.141	23.40637
Saimiri_Platy-1-1_NW_003943620.1_26400460:26402962_-	14.8	0.148	24.56839
Saimiri_Platy-1-1_NW_003943629.1_9540247:9542749_+	14.8	0.148	24.56839
Saimiri_Platy-1-1_NW_003943652.1_907418:909920_+	14.8	0.148	24.56839
Saimiri_Platy-1-1_NW_003943639.1_2973719:2976217_+	15.3	0.153	25.39841
Saimiri_Platy-1-1_NW_003943661.1_11515143:11517639_+	16.7	0.167	27.72244
Saimiri_Platy-1-1_NW_003943629.1_1276518:1279014_-	16.7	0.167	27.72244
Saimiri_Platy-1-1_NW_003943649.1_3252238:3254733_-	17.9	0.179	29.71448
Saimiri_Platy-1-1_NW_003943619.1_16386757:16389259_+	18.4	0.184	30.54449
Saimiri_Platy-1-1_NW_003943626.1_19068471:19070967_-	19.8	0.198	32.86853
Saimiri_Platy-1-1_NW_003943604.1_57673821:57676313_-	21.7	0.217	36.02258
Saimiri_Platy-1-1_NW_003943730.1_4856344:4858840_+	24	0.24	39.84064
Saimiri_Platy-1-2_NW_003943640.1_10141746:10144249_-	7.8	0.078	12.94821
Saimiri_Platy-1-2_NW_003943608.1_33150274:33152776_+	7.8	0.078	12.94821
Saimiri_Platy-1-2_NW_003943647.1_3154830:3157331_+	9	0.09	14.94024
Saimiri_Platy-1-2_NW_003943628.1_12640312:12642813_-	9.9	0.099	16.43426
Saimiri_Platy-1-2_NW_003943668.1_4933544:4936043_+	10.1	0.101	16.76627
Saimiri_Platy-1-2_NW_003943611.1_40873323:40875824_+	11	0.11	18.26029
Saimiri_Platy-1-2_NW_003943604.1_60226577:60229082_+	11.5	0.115	19.09031
Saimiri_Platy-1-2_NW_003943615.1_4726436:4728937_-	11.9	0.119	19.75432
Saimiri_Platy-1-2_NW_003943719.1_5144201:5146699_-	13.3	0.133	22.07835
Saimiri_Platy-1-2_NW_003943617.1_27784437:27786939_-	15.8	0.158	26.22842
Saimiri_Platy-1-2a_NW_003943604.1_16777125:16779615_+	4.5	0.045	7.47012
Saimiri_Platy-1-2a_NW_003943672.1_1960477:1962979_-	4.9	0.049	8.13413
Saimiri_Platy-1-2a_NW_003943726.1_2958133:2960635_-	5.9	0.059	9.794157

Saimiri_Platy-1-2a_NW_003943605.1_1706674:1709175_+	5.9	0.059	9.794157
Saimiri_Platy-1-2a_NW_003943752.1_1911401:1913903_+	6	0.06	9.960159
Saimiri_Platy-1-2a_NW_003943613.1_17609559:17612058_-	6.1	0.061	10.12616
Saimiri_Platy-1-2a_NW_003943607.1_22041517:22044005_-	6.8	0.068	11.28818
Saimiri_Platy-1-2a_NW_003943612.1_14496810:14499310_+	7	0.07	11.62019
Saimiri_Platy-1-2a_NW_003943707.1_4959345:4961847_-	7.8	0.078	12.94821
Saimiri_Platy-1-2a_NW_003943673.1_8631009:8633512_+	7.8	0.078	12.94821
Saimiri_Platy-1-2a_NW_003943725.1_5208988:5211490_+	8	0.08	13.28021
Saimiri_Platy-1-2a_NW_003943813.1_995714:998217_-	8.7	0.087	14.44223
Saimiri_Platy-1-2a_NW_003943667.1_11394513:11397016_+	8.7	0.087	14.44223
Saimiri_Platy-1-2a_NW_003944621.1_369:2870_+	8.9	0.089	14.77424
Saimiri_Platy-1-2a_NW_003943615.1_4512009:4514511_+	8.9	0.089	14.77424
Saimiri_Platy-1-2a_NW_003943613.1_8420620:8423116_+	9.5	0.095	15.77025
Saimiri_Platy-1-2a_NW_003943617.1_28176160:28178664_+	9.7	0.097	16.10226
Saimiri_Platy-1-2a_NW_003943676.1_1145974:1148476_+	9.9	0.099	16.43426
Saimiri_Platy-1-2a_NW_003943693.1_7742373:7744875_+	10	0.1	16.60027
Saimiri_Platy-1-2a_NW_003943685.1_153557:156059_+	10.8	0.108	17.92829
Saimiri_Platy-1-2a_NW_003943613.1_40895073:40897576_+	10.8	0.108	17.92829
Saimiri_Platy-1-2a_NW_003943625.1_19461289:19463790_-	12.9	0.129	21.41434
Saimiri_Platy-1-2a_NW_003943622.1_21555216:21557737_+	12.9	0.129	21.41434
Saimiri_Platy-1-2a_NW_003943640.1_12744655:12747155_-	13	0.13	21.58035
Saimiri_Platy-1-2a_NW_003943610.1_45240745:45243246_+	13	0.13	21.58035
Saimiri_Platy-1-2a_NW_003943611.1_20662456:20664940_-	15.5	0.155	25.73041
Saimiri_Platy-1-2a_NW_003943605.1_46827113:46829615_-	15.7	0.157	26.06242
Saimiri_Platy-1-2a_NW_003943621.1_17550230:17552734_+	18.2	0.182	30.21248
Saimiri_Platy-1-2b_NW_003943655.1_2452395:2454897_+	7.1	0.071	11.78619
Saimiri_Platy-1-2b_NW_003943639.1_6652985:6655486_+	7.2	0.072	11.95219
Saimiri_Platy-1-2b_NW_003943657.1_6905863:6908358_+	8.7	0.087	14.44223
Saimiri_Platy-1-2b_NW_003943639.1_5773822:5776322_-	9	0.09	14.94024
Saimiri_Platy-1-2b_NW_003943607.1_42148989:42151491_+	9.9	0.099	16.43426
Saimiri_Platy-1-2b_NW_003943619.1_23377500:23380012_-	10.1	0.101	16.76627
Saimiri_Platy-1-2b_NW_003943753.1_1319670:1322171_+	10.2	0.102	16.93227
Saimiri_Platy-1-2b_NW_003943731.1_3478231:3480734_+	11.7	0.117	19.42231
Saimiri_Platy-1-2b_NW_003943654.1_4273134:4275628_-	11.7	0.117	19.42231
Saimiri_Platy-1-2b_NW_003943618.1_2385078:2387581_-	11.8	0.118	19.58831
Saimiri_Platy-1-2b_NW_003943653.1_1044085:1046587_+	12.8	0.128	21.24834
Saimiri_Platy-1-2b_NW_003943617.1_9915545:9918044_+	13.1	0.131	21.74635
Saimiri_Platy-1-2b_NW_003943605.1_70388285:70390795_+	13.3	0.133	22.07835
Saimiri_Platy-1-2b_NW_003943609.1_22239272:22241773_+	13.5	0.135	22.41036
Saimiri_Platy-1-2b_NW_003943645.1_12865803:12868305_+	13.9	0.139	23.07437
Saimiri_Platy-1-2b_NW_003943708.1_3128326:3130828_+	16.7	0.167	27.72244

Saimiri_Platy-1-2b_NW_003943612.1_10848863:10851364_-	18.2	0.182	30.21248
Saimiri_Platy-1-2b_NW_003943649.1_11996235:11998737_+	18.6	0.186	30.87649
Saimiri_Platy-1-2b_NW_003943641.1_3254251:3256744_+	24.7	0.247	41.00266
Saimiri_Platy-1-3_NW_003943611.1_44125674:44128175_+	5	0.05	8.300133
Saimiri_Platy-1-3_NW_003943605.1_87472:89970_+	6.1	0.061	10.12616
Saimiri_Platy-1-3_NW_003943609.1_41039838:41042339_+	6.9	0.069	11.45418
Saimiri_Platy-1-3_NW_003943650.1_6878739:6881242_+	7.4	0.074	12.2842
Saimiri_Platy-1-3_NW_003943615.1_25960099:25962602_-	7.8	0.078	12.94821
Saimiri_Platy-1-3_NW_003943606.1_32959832:32962334_-	7.9	0.079	13.11421
Saimiri_Platy-1-3_NW_003943650.1_1349453:1351948_-	8.6	0.086	14.27623
Saimiri_Platy-1-3_NW_003943622.1_22090956:22093458_+	8.9	0.089	14.77424
Saimiri_Platy-1-3_NW_003943608.1_17424183:17426686_+	9	0.09	14.94024
Saimiri_Platy-1-3_NW_003943691.1_3233362:3235876_+	9.2	0.092	15.27224
Saimiri_Platy-1-3_NW_003943716.1_6046365:6048868_+	9.7	0.097	16.10226
Saimiri_Platy-1-3_NW_003943713.1_6717356:6719858_-	9.9	0.099	16.43426
Saimiri_Platy-1-3_NW_003943795.1_1009829:1012329_-	10	0.1	16.60027
Saimiri_Platy-1-3_NW_003943669.1_11035183:11037682_+	10.1	0.101	16.76627
Saimiri_Platy-1-3_NW_003943641.1_18384097:18386599_+	10.9	0.109	18.09429
Saimiri_Platy-1-3_NW_003943604.1_507341:509851_+	11	0.11	18.26029
Saimiri_Platy-1-3_NW_003943738.1_4204344:4206850_-	11.8	0.118	19.58831
Saimiri_Platy-1-3_NW_003943705.1_5153679:5156180_+	12	0.12	19.92032
Saimiri_Platy-1-3_NW_003943667.1_5219474:5221976_+	12.2	0.122	20.25232
Saimiri_Platy-1-3_NW_003943616.1_2347350:2349855_-	12.4	0.124	20.58433
Saimiri_Platy-1-3_NW_003943629.1_11708465:11710967_-	15.7	0.157	26.06242
Saimiri_Platy-1-4a_NW_003943606.1_6781032:6783535_-	1.9	0.019	3.15405
Saimiri_Platy-1-4a_NW_003943612.1_6461750:6464248_+	3.1	0.031	5.146082
Saimiri_Platy-1-4a_NW_003943738.1_1401730:1404229_+	4	0.04	6.640106
Saimiri_Platy-1-4a_NW_003943626.1_18658328:18660831_-	4.8	0.048	7.968127
Saimiri_Platy-1-4a_NW_003943699.1_8331458:8333961_+	4.8	0.048	7.968127
Saimiri_Platy-1-4a_NW_003943684.1_138807:141309_+	5	0.05	8.300133
Squirrel_Platy-1-4a_NW_003943612.1:39478956-39480257_-	5.1	0.051	8.466135
Saimiri_Platy-1-4a_NW_003943615.1_33512912:33515413_+	5.2	0.052	8.632138
Saimiri_Platy-1-4a_NW_003943612.1_28521219:28523722_+	5.8	0.058	9.628154
Saimiri_Platy-1-4a_NW_003943622.1_241459:243960_-	5.9	0.059	9.794157
Saimiri_Platy-1-4a_NW_003943606.1_42900461:42902965_+	5.9	0.059	9.794157
Squirrel_Platy-1-4a_NW_003943747.1:4217089-4218390_-	6.2	0.062	10.29216
Saimiri_Platy-1-4a_NW_003943613.1_7454659:7457155_-	6.2	0.062	10.29216
Saimiri_Platy-1-4a_NW_003943672.1_6665380:6667883_-	6.8	0.068	11.28818
Saimiri_Platy-1-4a_NW_003943775.1_529291:531791_+	7	0.07	11.62019
Saimiri_Platy-1-4a_NW_003943731.1_5641960:5644462_+	7	0.07	11.62019
Saimiri_Platy-1-4a_NW_003943730.1_2076678:2079181_-	7.8	0.078	12.94821

Squirrel_Platy-1-4a_NW_003943604.1:36625130-36626429_+	7.9	0.079	13.11421
Saimiri_Platy-1-4a_NW_003943645.1_2692074:2694576_-	7.9	0.079	13.11421
Saimiri_Platy-1-4a_NW_003943651.1_16375904:16378407_+	8.1	0.081	13.44622
Saimiri_Platy-1-4a_NW_003943641.1_11631192:11633695_+	8.1	0.081	13.44622
Squirrel_Platy-1-4a_NW_003943657.1:328883-330184_-	8.1	0.081	13.44622
Saimiri_Platy-1-4a_NW_003943647.1_15115940:15118438_+	8.5	0.085	14.11023
Saimiri_Platy-1-4a_NW_003943648.1_16369238:16371741_-	8.7	0.087	14.44223
Squirrel_Platy-1-4a_NW_003943781.1:184332-185635_-	8.9	0.089	14.77424
Squirrel_Platy-1-4a_NW_003943610.1:40063113-40064416_-	9	0.09	14.94024
Squirrel_Platy-1-4a_NW_003943618.1:30586949-30588244_-	9	0.09	14.94024
Saimiri_Platy-1-4a_NW_003943799.1_442780:445281_+	9	0.09	14.94024
Saimiri_Platy-1-4a_NW_003943692.1_4280787:4283291_+	9.6	0.096	15.93625
Saimiri_Platy-1-4a_NW_003943776.1_3243627:3246130_-	9.7	0.097	16.10226
Squirrel_Platy-1-4a_NW_003943755.1:2193939-2195242_+	9.7	0.097	16.10226
Saimiri_Platy-1-4a_NW_003943614.1_35275004:35277504_-	10	0.1	16.60027
Squirrel_Platy-1-4a_NW_003943630.1:1636470-1637773_-	10.1	0.101	16.76627
Saimiri_Platy-1-4a_NW_003943654.1_11837288:11839791_+	10.1	0.101	16.76627
Saimiri_Platy-1-4a_NW_003943821.1_310350:312854_+	10.8	0.108	17.92829
Saimiri_Platy-1-4a_NW_003943785.1_1384091:1386594_+	10.9	0.109	18.09429
Saimiri_Platy-1-4a_NW_003943609.1_39780442:39782925_-	11	0.11	18.26029
Saimiri_Platy-1-4a_NW_003943613.1_14285384:14287887_-	11.8	0.118	19.58831
Squirrel_Platy-1-4a_NW_003943621.1:11180851-11182155_-	11.8	0.118	19.58831
Saimiri_Platy-1-4a_NW_003943712.1_1182440:1184941_-	12	0.12	19.92032
Saimiri_Platy-1-4a_NW_003943680.1_1365382:1367877_+	12.3	0.123	20.41833
Saimiri_Platy-1-4a_NW_003943699.1_648069:650572_+	12.8	0.128	21.24834
Saimiri_Platy-1-4a_NW_003943622.1_25047946:25050449_+	15.5	0.155	25.73041
Saimiri_Platy-1-5_NW_003943622.1_23791093:23793600_-	4.7	0.047	7.802125
Saimiri_Platy-1-5_NW_003943650.1_7244030:7246535_-	6.7	0.067	11.12218
Saimiri_Platy-1-5_NW_003943812.1_911423:913929_-	7.5	0.075	12.4502
Saimiri_Platy-1-5_NW_003943819.1_772355:774860_-	7.6	0.076	12.6162
Saimiri_Platy-1-5_NW_003943673.1_494026:496531_-	7.6	0.076	12.6162
Saimiri_Platy-1-5_NW_003943606.1_46936654:46939159_+	7.6	0.076	12.6162
Saimiri_Platy-1-5_NW_003943614.1_42378159:42380663_-	7.8	0.078	12.94821
Squirrel_Platy-1-5_NW_003943614.1:14191580-14192885_-	8.1	0.081	13.44622
Saimiri_Platy-1-5_NW_003943802.1_356546:359051_+	8.6	0.086	14.27623
Saimiri_Platy-1-5_NW_003943654.1_1650332:1652835_-	9	0.09	14.94024
Saimiri_Platy-1-5_NW_003943656.1_12898801:12901302_+	9.3	0.093	15.43825
Saimiri_Platy-1-5_NW_003943638.1_14427140:14429645_+	10.5	0.105	17.43028
Saimiri_Platy-1-5_NW_003943642.1_4552296:4554798_+	14	0.14	23.24037
Saimiri_Platy-1-5_NW_003943608.1_10407564:10410066_-	17.6	0.176	29.21647

Table A2.14 Owl monkey Platy-1 percent divergence. Green highlight indicates a predicted lineage-specific insertion; yellow highlight indicates a predicated lineage-specific insertion that was PCR-analyzed.

Locus	% divergence	Percent	Age (my)
Owl_Platy-1-1_NW_012169090.1:2936043-2936147	4.9	0.049	8.13413
Owl_Platy-1-1_NW_012184613.1:35624-35725	6.3	0.063	10.45817
Owl_Platy-1-1_NW_012184214.1:362956-363057	9	0.09	14.94024
Owl_Platy-1-1_NW_012190534.1:2718459-2718561	9	0.09	14.94024
Owl_Platy-1-1_NW_012171312.1:20970867-20970964	9.3	0.093	15.43825
Owl_Platy-1-1_NW_012188868.1:1181349-1181444	9.5	0.095	15.77025
Owl_Platy-1-1_NW_012162423.1:297662-297764	9.8	0.098	16.26826
Owl_Platy-1-1_NW_012178646.1:2680516-2680618	10	0.1	16.60027
Owl_Platy-1-1_NW_012173534.1:35510993-35511095	10.1	0.101	16.76627
Owl_Platy-1-1_NW_012189424.1:4323675-4323776	10.1	0.101	16.76627
Owl_Platy-1-1_NW_012177091.1:4861138-4861239	10.9	0.109	18.09429
Owl_Platy-1-1_NW_012185580.1:140372-140475	10.9	0.109	18.09429
Owl_Platy-1-1_NW_012184014.1:3026926-3027028	11	0.11	18.26029
Owl_Platy-1-1_NW_012176869.1:3371276-3371372	11.5	0.115	19.09031
Owl_Platy-1-1_NW_012163535.1:17840672-17840775	11.7	0.117	19.42231
Owl_Platy-1-1_NW_012170424.1:1923383-1923479	11.7	0.117	19.42231
Owl_Platy-1-1_NW_012172090.1:2495021-2495123	11.8	0.118	19.58831
Owl_Platy-1-1_NW_012177646.1:3483493-3483595	11.9	0.119	19.75432
Owl_Platy-1-1_NW_012183958.1:1467542-1467644	12.8	0.128	21.24834
Owl_Platy-1-1_NW_012189090.1:4979-5081	12.8	0.128	21.24834
Owl_Platy-1-1_NW_012190979.1:226149-226251	12.8	0.128	21.24834
Owl_Platy-1-1_NW_012171090.1:5891644-5891740	13.5	0.135	22.41036
Owl_Platy-1-1_NW_012184646.1:7676266-7676369	13.6	0.136	22.57636
Owl_Platy-1-1_NW_012189423.1:15745547-15745650	13.8	0.138	22.90837
Owl_Platy-1-1_NW_012163536.1:4639642-4639750	14	0.14	23.24037
Owl_Platy-1-1_NW_012184536.1:153415-153517	14	0.14	23.24037
Owl_Platy-1-1_NW_012184647.1:1726034-1726130	14.6	0.146	24.23639
Owl_Platy-1-1_NW_012170313.1:3433074-3433177	14.7	0.147	24.40239
Owl_Platy-1-1_NW_012177979.1:1063515-1063617	14.7	0.147	24.40239
Owl_Platy-1-1_NW_012184979.1:12918014-12918109	14.7	0.147	24.40239
Owl_Platy-1-1_NW_012187946.1:159185-159289	15.3	0.153	25.39841
Owl_Platy-1-1_NW_012185646.1:8032445-8032548	15.5	0.155	25.73041
Owl_Platy-1-1_NW_012175091.1:2824488-2824584	15.6	0.156	25.89641
Owl_Platy-1-1_NW_012171312.1:22155786-22155882	17.7	0.177	29.38247
Owl_Platy-1-1_NW_012186313.1:6630887-6630980	17.9	0.179	29.71448
Owl_Platy-1-1_NW_012189423.1:4918817-4918909	18	0.18	29.88048

Owl_Platy-1-1_NW_012163313.1:4968465-4968561	18.1	0.181	30.04648
Owl_Platy-1-1_NW_012184746.1:459257-459352	20	0.2	33.20053
Owl_Platy-1-1_NW_012187646.1:6844533-6844629	20.2	0.202	33.53254
Owl_Platy-1-1_NW_012187757.1:3664183-3664280	20.8	0.208	34.52855
Owl_Platy-1-1_NW_012186090.1:220253-220358	20.9	0.209	34.69456
Owl_Platy-1-1_NW_012163535.1:32779466-32779562	21.9	0.219	36.35458
Owl_Platy-1-2_NW_012169090.1:1671054-1671156	4.9	0.049	8.13413
Owl_Platy-1-2_NW_012165424.1:1353852-1353953	5	0.05	8.300133
Owl_Platy-1-2_NW_012184980.1:5757693-5757795	5.9	0.059	9.794157
Owl_Platy-1-2_NW_012172535.1:907776-907879	6	0.06	9.960159
Owl_Platy-1-2_NW_012164091.1:2690652-2690754	6.9	0.069	11.45418
Owl_Platy-1-2_NW_012189423.1:1258401-1258502	6.9	0.069	11.45418
Owl_Platy-1-2_NW_012164091.1:2680679-2680781	6.9	0.069	11.45418
Owl_Platy-1-2_NW_012190868.1:9321119-9321220	7.9	0.079	13.11421
Owl_Platy-1-2_NW_012173534.1:7938480-7938592	8.1	0.081	13.44622
Owl_Platy-1-2_NW_012184158.1:1941390-1941491	8.2	0.082	13.61222
Owl_Platy-1-2_NW_012184202.1:1675442-1675544	8.9	0.089	14.77424
Owl_Platy-1-2_NW_012187325.1:436538-436640	9	0.09	14.94024
Owl_Platy-1-2_NW_012189757.1:6058125-6058226	9	0.09	14.94024
Owl_Platy-1-2_NW_012189423.1:10665969-10666070	9.1	0.091	15.10624
Owl_Platy-1-2_NW_012187202.1:2108111-2108214	9.7	0.097	16.10226
Owl_Platy-1-2_NW_012169535.1:1490323-1490425	9.9	0.099	16.43426
Owl_Platy-1-2_NW_012189424.1:9077005-9077107_former_2a	10.2	0.102	16.93227
Owl_Platy-1-2_NW_012188646.1:2153921-2154023	11	0.11	18.26029
Owl_Platy-1-2_NW_012172423.1:2174788-2174895	11.8	0.118	19.58831
Owl_Platy-1-2_NW_012176424.1:2649633-2649735	11.8	0.118	19.58831
Owl_Platy-1-2_NW_012185302.1:161199-161300	11.9	0.119	19.75432
Owl_Platy-1-2_NW_012187201.1:6013312-6013413	12.9	0.129	21.41434
Owl_Platy-1-2a_NW_012184868.1:5356998-5357100	4	0.04	6.640106
Owl_Platy-1-2a_NW_012164202.1:3713235-3713337	4.1	0.041	6.806109
Owl_Platy-1-2a_NW_012171312.1:11079817-11079907	4.5	0.045	7.47012
Owl_Platy-1-2a_NW_012176424.1:1014868-1014970	4.9	0.049	8.13413
Owl_Platy-1-2a_NW_012184025.1:1425427-1425529	4.9	0.049	8.13413
Owl_Platy-1-2a_NW_012184802.1:527633-527734	5.9	0.059	9.794157
Owl_Platy-1-2a_NW_012185313.1:4572561-4572663	5.9	0.059	9.794157
Owl_Platy-1-2a_NW_012187269.1:86082-86184	6	0.06	9.960159
Owl_Platy-1-2a_NW_012162647.1:5295557-5295658	6.9	0.069	11.45418
Owl_Platy-1-2a_NW_012167424.1:713817-713919	7.8	0.078	12.94821
Owl_Platy-1-2a_NW_012185025.1:815826-815928	7.8	0.078	12.94821
Owl_Platy-1-2a_NW_012191312.1:2658383-2658485	7.8	0.078	12.94821
Owl_Platy-1-2a_NW_012173535.1:9675578-9675680	7.9	0.079	13.11421

Owl_Platy-1-2a_NW_012188312.1:22035293-22035381	8	0.08	13.28021
Owl_Platy-1-2a_NW_012184757.1:4571605-4571706	8.1	0.081	13.44622
Owl_Platy-1-2a_NW_012170868.1:3906449-3906551	8.2	0.082	13.61222
Owl_Platy-1-2a_NW_012183869.1:1597938-1598041	9.7	0.097	16.10226
Owl_Platy-1-2a_NW_012173534.1:4251338-4251440	9.8	0.098	16.26826
Owl_Platy-1-2a_NW_012184091.1:5783399-5783501	9.8	0.098	16.26826
Owl_Platy-1-2a_NW_012172535.1:1491730-1491843	10	0.1	16.60027
Owl_Platy-1-2a_NW_012189423.1:12523505-12523609	10	0.1	16.60027
Owl_Platy-1-2a_NW_012167868.1:895285-895388	10.9	0.109	18.09429
Owl_Platy-1-2a_NW_012176868.1:10959883-10959984	10.9	0.109	18.09429
Owl_Platy-1-2a_NW_012178424.1:875661-875762	10.9	0.109	18.09429
Owl_Platy-1-2a_NW_012163869.1:6833867-6833966	11.1	0.111	18.42629
Owl_Platy-1-2a_NW_012179535.1:1101992-1102089	11.3	0.113	18.7583
Owl_Platy-1-2a_NW_012184857.1:1202649-1202751	11.8	0.118	19.58831
Owl_Platy-1-2a_NW_012184358.1:87439-87540	11.9	0.119	19.75432
Owl_Platy-1-2a_NW_012186868.1:3979986-3980088	11.9	0.119	19.75432
Owl_Platy-1-2a_NW_012187424.1:6175739-6175841	12.2	0.122	20.25232
Owl_Platy-1-2a_NW_012165424.1:1861624-1861709	12.9	0.129	21.41434
Owl_Platy-1-2a_NW_012167646.1:10178296-10178398	13.3	0.133	22.07835
Owl_Platy-1-2a_NW_012164424.1:6158658-6158765	14.2	0.142	23.57238
Owl_Platy-1-2a_NW_012188646.1:2664100-2664201	14.8	0.148	24.56839
Owl_Platy-1-2a_NW_012177979.1:9460910-9461013	15.8	0.158	26.22842
Owl_Platy-1-2a_NW_012184202.1:12816413-12816517	17.3	0.173	28.71846
Owl_Platy-1-2a_NW_012189312.1:9461610-9461719	19.1	0.191	31.70651
Owl_Platy-1-2b_NW_012183868.1:7418903-7419005	5.9	0.059	9.794157
Owl_Platy-1-2b_NW_012191312.1:2401975-2402077	5.9	0.059	9.794157
Owl_Platy-1-2b_NW_012182423.1:7347324-7347426	6.1	0.061	10.12616
Owl_Platy-1-2b_NW_012189090.1:5283619-5283719	7	0.07	11.62019
Owl_Platy-1-2b_NW_012166091.1:5131406-5131507	7.9	0.079	13.11421
Owl_Platy-1-2b_NW_012165980.1:1672334-1672447	8.1	0.081	13.44622
Owl_Platy-1-2b_NW_012167202.1:5072145-5072238	8.5	0.085	14.11023
Owl_Platy-1-2b_NW_012190534.1:27424763-27424866	8.7	0.087	14.44223
Owl_Platy-1-2b_NW_012185114.1:1027050-1027150	9.1	0.091	15.10624
Owl_Platy-1-2b_NW_012184424.1:3175688-3175776	9.2	0.092	15.27224
Owl_Platy-1-2b_NW_012180868.1:643914-644009	9.8	0.098	16.26826
Owl_Platy-1-2b_NW_012183869.1:11884061-11884145	9.9	0.099	16.43426
Owl_Platy-1-2b_NW_012189757.1:6380845-6380947	10	0.1	16.60027
Owl_Platy-1-2b_NW_012173534.1:23041770-23041873	10.7	0.107	17.76228
Owl_Platy-1-2b_NW_012190646.1:312136-312239	10.7	0.107	17.76228
Owl_Platy-1-2b_NW_012180543.1:1009-1124	10.8	0.108	17.92829
Owl_Platy-1-2b_NW_012169313.1:3109347-3109448	10.9	0.109	18.09429

Owl_Platy-1-2b_NW_012181646.1:789377-789479	10.9	0.109	18.09429
Owl_Platy-1-2b_NW_012188646.1:1667120-1667225	11	0.11	18.26029
Owl_Platy-1-2b_NW_012186202.1:4485474-4485576	11.8	0.118	19.58831
Owl_Platy-1-2b_NW_012186424.1:3482995-3483098	11.8	0.118	19.58831
Owl_Platy-1-2b_NW_012166313.1:3251450-3251551	12	0.12	19.92032
Owl_Platy-1-2b_NW_012172201.1:958455-958557	12	0.12	19.92032
Owl_Platy-1-2b_NW_012167313.1:2947531-2947633	12.8	0.128	21.24834
Owl_Platy-1-2b_NW_012188090.1:1455938-1456040	12.8	0.128	21.24834
Owl_Platy-1-2b_NW_012165757.1:2715535-2715637	13	0.13	21.58035
Owl_Platy-1-2b_NW_012186090.1:11976586-11976674	13.1	0.131	21.74635
Owl_Platy-1-2b_NW_012187424.1:5967683-5967785	13.7	0.137	22.74236
Owl_Platy-1-2b_NW_012166535.1:5728877-5728979	13.9	0.139	23.07437
Owl_Platy-1-2b_NW_012173535.1:297312-297414	13.9	0.139	23.07437
Owl_Platy-1-2b_NW_012186313.1:7737378-7737475	14.4	0.144	23.90438
Owl_Platy-1-2b_NW_012174646.1:7972408-7972504	14.6	0.146	24.23639
Owl_Platy-1-2b_NW_012175796.1:638-731	14.8	0.148	24.56839
Owl_Platy-1-2b_NW_012188757.1:8687044-8687130	14.8	0.148	24.56839
Owl_Platy-1-2b_NW_012173534.1:26439184-26439277	15.1	0.151	25.0664
Owl_Platy-1-2b_NW_012189423.1:12926490-12926590	15.2	0.152	25.2324
Owl_Platy-1-2b_NW_012183534.1:1895901-1896001	15.3	0.153	25.39841
Owl_Platy-1-2b_NW_012188090.1:1622967-1623069	15.3	0.153	25.39841
Owl_Platy-1-2b_NW_012165757.1:1879386-1879481	15.8	0.158	26.22842
Owl_Platy-1-2b_NW_012166868.1:4843111-4843213	17.9	0.179	29.71448
Owl_Platy-1-2b_NW_012183534.1:11167223-11167325_former_6	18.9	0.189	31.3745
Owl_Platy-1-2b_NW_012162425.1:6193202-6193305	20.6	0.206	34.19655
Owl_Platy-1-3_NW_012181868.1:105555-105649	3.2	0.032	5.312085
Owl_Platy-1-3_NW_012178646.1:4253641-4253742	5	0.05	8.300133
Owl_Platy-1-3_NW_012165535.1:1469690-1469792	5.9	0.059	9.794157
Owl_Platy-1-3_NW_012165198.1:5928-6031	6.8	0.068	11.28818
Owl_Platy-1-3_NW_012164869.1:6084935-6085037	6.9	0.069	11.45418
Owl_Platy-1-3_NW_012162423.1:14651621-14651723	6.9	0.069	11.45418
Owl_Platy-1-3_NW_012163202.1:301986-302082	7.3	0.073	12.11819
Owl_Platy-1-3_NW_012183892.1:2132951-2133053	7.9	0.079	13.11421
Owl_Platy-1-3_NW_012186720.1:3413-3514	7.9	0.079	13.11421
Owl_Platy-1-3_NW_012191423.1:6797949-6798050	7.9	0.079	13.11421
Owl_Platy-1-3_NW_012167535.1:5648112-5648215	8.7	0.087	14.44223
Owl_Platy-1-3_NW_012174424.1:289948-290051	8.7	0.087	14.44223
Owl_Platy-1-3_NW_012163091.1:1445425-1445528	8.8	0.088	14.60823
Owl_Platy-1-3_NW_012170535.1:467459-467561	8.8	0.088	14.60823
Owl_Platy-1-3_NW_012185535.1:12734648-12734750	8.8	0.088	14.60823
Owl_Platy-1-3_NW_012185757.1:6679198-6679300	8.8	0.088	14.60823

Owl_Platy-1-3_NW_012170313.1:1254415-1254517	8.9	0.089	14.77424
Owl_Platy-1-3_NW_012184092.1:478613-478716	9	0.09	14.94024
Owl_Platy-1-3_NW_012186757.1:6012082-6012184	9.2	0.092	15.27224
Owl_Platy-1-3_NW_012173534.1:14650485-14650568	9.6	0.096	15.93625
Owl_Platy-1-3_NW_012184003.1:2131102-2131198	10.5	0.105	17.43028
Owl_Platy-1-3_NW_012179646.1:1367433-1367528	10.6	0.106	17.59628
Owl_Platy-1-3_NW_012179646.1:1376591-1376686	10.8	0.108	17.92829
Owl_Platy-1-3_NW_012174202.1:5832024-5832125	11.1	0.111	18.42629
Owl_Platy-1-3_NW_012188458.1:41468-41554	11.6	0.116	19.25631
Owl_Platy-1-3_NW_012173534.1:34177735-34177842	12.6	0.126	20.91633
Owl_Platy-1-3_NW_012185313.1:8178519-8178618	12.8	0.128	21.24834
Owl_Platy-1-3_NW_012180757.1:2213796-2213897	13	0.13	21.58035
Owl_Platy-1-3_NW_012184092.1:29931-30032	13.9	0.139	23.07437
Owl_Platy-1-3_NW_012188090.1:3823253-3823355	13.9	0.139	23.07437
Owl_Platy-1-4_NW_012189423.1:11596853-11596955	4.9	0.049	8.13413
Owl_Platy-1-4_NW_012189868.1:4852387-4852489	5	0.05	8.300133
Owl_Platy-1-4_NW_012173980.1:2013756-2013857	6.2	0.062	10.29216
Owl_Platy-1-4_NW_012190201.1:5670600-5670702	7.8	0.078	12.94821
Owl_Platy-1-4a_NW_012186114.1:246267-246369	0.9	0.009	1.494024
Owl_Platy-1-4a_NW_012176646.1:1884707-1884807	1	0.01	1.660027
Owl_Platy-1-4a_NW_012184980.1:7322676-7322777	2	0.02	3.320053
Owl_Platy-1-4a_NW_012190757.1:6050455-6050556	2	0.02	3.320053
Owl_Platy-1-4a_NW_012169313.1:2654614-2654716	2.9	0.029	4.814077
Owl_Platy-1-4a_NW_012183869.1:13603007-13603109	2.9	0.029	4.814077
Owl_Platy-1-4a_NW_012185913.1:188266-188368	2.9	0.029	4.814077
Owl_Platy-1-4a_NW_012173201.1:4719503-4719604	3	0.03	4.98008
Owl_Platy-1-4a_NW_012185757.1:11543495-11543596	3.1	0.031	5.146082
Owl_Platy-1-4a_NW_012164202.1:2548324-2548426	3.9	0.039	6.474104
Owl_Platy-1-4a_NW_012165980.1:3779363-3779466	3.9	0.039	6.474104
Owl_Platy-1-4a_NW_012168979.1:8062006-8062108	3.9	0.039	6.474104
Owl_Platy-1-4a_NW_012183813.1:552683-552786	3.9	0.039	6.474104
Owl_Platy-1-4a_NW_012184269.1:121958-122061	3.9	0.039	6.474104
Owl_Platy-1-4a_NW_012188868.1:4269080-4269182	3.9	0.039	6.474104
Owl_Platy-1-4a_NW_012163535.1:23826465-23826567	4	0.04	6.640106
Owl_Platy-1-4a_NW_012165757.1:4481704-4481810	4	0.04	6.640106
Owl_Platy-1-4a_NW_012165757.1:4482954-4483060	4	0.04	6.640106
Owl_Platy-1-4a_NW_012178091.1:1955069-1955170	4	0.04	6.640106
Owl_Platy-1-4a_NW_012168313.1:1440075-1440173	4.1	0.041	6.806109
Owl_Platy-1-4a_NW_012164424.1:2374501-2374604	4.8	0.048	7.968127
Owl_Platy-1-4a_NW_012176535.1:1424981-1425084	4.8	0.048	7.968127
Owl_Platy-1-4a_NW_012184047.1:98567-98670	4.8	0.048	7.968127

Owl_Platy-1-4a_NW_012190534.1:17651049-17651154	4.8	0.048	7.968127
Owl_Platy-1-4a_NW_012165535.1:11528217-11528319	4.9	0.049	8.13413
Owl_Platy-1-4a_NW_012176313.1:304188-304290	4.9	0.049	8.13413
Owl_Platy-1-4a_NW_012183869.1:10417195-10417299	4.9	0.049	8.13413
Owl_Platy-1-4a_NW_012184735.1:1484696-1484798	4.9	0.049	8.13413
Owl_Platy-1-4a_NW_012170201.1:10537781-10537881	5	0.05	8.300133
Owl_Platy-1-4a_NW_012171201.1:132016-132118	5	0.05	8.300133
Owl_Platy-1-4a_NW_012173312.1:2571500-2571602	5	0.05	8.300133
Owl_Platy-1-4a_NW_012174424.1:747701-747803	5	0.05	8.300133
Owl_Platy-1-4a_NW_012183881.1:120112-120213	5	0.05	8.300133
Owl_Platy-1-4a_NW_012184535.1:3014663-3014764	5	0.05	8.300133
Owl_Platy-1-4a_NW_012185202.1:862626-862727	5	0.05	8.300133
Owl_Platy-1-4a_NW_012185757.1:12425680-12425782	5	0.05	8.300133
Owl_Platy-1-4a_NW_012185957.1:947992-948094	5	0.05	8.300133
Owl_Platy-1-4a_NW_012189979.1:3723206-3723309	5	0.05	8.300133
Owl_Platy-1-4a_NW_012168424.1:4326975-4327054	5.1	0.051	8.466135
Owl_Platy-1-4a_NW_012169090.1:2106432-2106529	5.2	0.052	8.632138
Owl_Platy-1-4a_NW_012183869.1:5673654-5673751	5.2	0.052	8.632138
Owl_Platy-1-4a_NW_012186979.1:9295301-9295403	5.2	0.052	8.632138
Owl_Platy-1-4a_NW_012169535.1:728076-728169	5.4	0.054	8.964143
Owl_Platy-1-4a_NW_012185247.1:61159-61250	5.5	0.055	9.130146
Owl_Platy-1-4a_NW_012167424.1:2226313-2226416	5.8	0.058	9.628154
Owl_Platy-1-4a_NW_012189201.1:2745099-2745204	5.8	0.058	9.628154
Owl_Platy-1-4a_NW_012162869.1:5364835-5364937	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012162869.1:5365402-5365504	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012163158.1:19298-19400	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012163980.1:1247380-1247482	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012167313.1:3173858-3173960	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012167868.1:6778941-6779043	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012173758.1:3202752-3202854	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012174646.1:11019755-11019857	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012176202.1:1353996-1354098	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012178535.1:1006791-1006893	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012183201.1:322481-322583	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012183802.1:781164-781267	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012183824.1:1101850-1101952	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012184480.1:863884-863986	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012185313.1:10777159-10777261	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012185458.1:2034965-2035067	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012186646.1:6551975-6552077	5.9	0.059	9.794157
Owl_Platy-1-4a_NW_012186757.1:11668553-11668655	5.9	0.059	9.794157

Owl_Platy-1-4a_NW_012169090.1:4300281-4300383_former_3	6	0.06	9.960159
Owl_Platy-1-4a_NW_012173758.1:328227-328329	6	0.06	9.960159
Owl_Platy-1-4a_NW_012185313.1:9239070-9239171	6	0.06	9.960159
Owl_Platy-1-4a_NW_012165091.1:556436-556538	6.1	0.061	10.12616
Owl_Platy-1-4a_NW_012178757.1:4217025-4217127	6.1	0.061	10.12616
Owl_Platy-1-4a_NW_012186757.1:1875049-1875151	6.1	0.061	10.12616
Owl_Platy-1-4a_NW_012187202.1:5070688-5070788	6.1	0.061	10.12616
Owl_Platy-1-4a_NW_012188090.1:6532176-6532269	6.5	0.065	10.79017
Owl_Platy-1-4a_NW_012164646.1:14561885-14561978	6.6	0.066	10.95618
Owl_Platy-1-4a_NW_012184702.1:24227-24330	6.8	0.068	11.28818
Owl_Platy-1-4a_NW_012186091.1:6351397-6351500	6.8	0.068	11.28818
Owl_Platy-1-4a_NW_012182535.1:1154011-1154113	6.9	0.069	11.45418
Owl_Platy-1-4a_NW_012186313.1:4701910-4702012	6.9	0.069	11.45418
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Owl_Platy-1-4a_NW_012189424.1:1588402-1588504	6.9	0.069	11.45418
Owl_Platy-1-4a_NW_012189979.1:1974646-1974750	6.9	0.069	11.45418
Owl_Platy-1-4a_NW_012190868.1:3122816-3122917	6.9	0.069	11.45418
Owl_Platy-1-4a_NW_012171126.1:2521-2623	7	0.07	11.62019
Owl_Platy-1-4a_NW_012171312.1:5539931-5540033	7	0.07	11.62019
Owl_Platy-1-4a_NW_012185424.1:2354464-2354566	7	0.07	11.62019
Owl_Platy-1-4a_NW_012162647.1:5343565-5343664	7.1	0.071	11.78619
Owl_Platy-1-4a_NW_012176757.1:2674742-2674841	7.1	0.071	11.78619
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Owl_Platy-1-4a_NW_012168646.1:1504685-1504787	7.8	0.078	12.94821
Owl_Platy-1-4a_NW_012175646.1:4412152-4412254	7.8	0.078	12.94821
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Owl_Platy-1-4a_NW_012191423.1:5463739-5463841	6.9	0.069	11.45418
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Owl_Platy-1-4b_NW_012169313.1:3048113-3048215_former_4	1	0.01	1.660027
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Owl_Platy-1-4b3_NW_012184424.1:3053839-3053941_former_4	1	0.01	1.660027
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Owl_Platy-1-4b3_NW_012185158.1:1005451-1005553_former_4	2.9	0.029	4.814077
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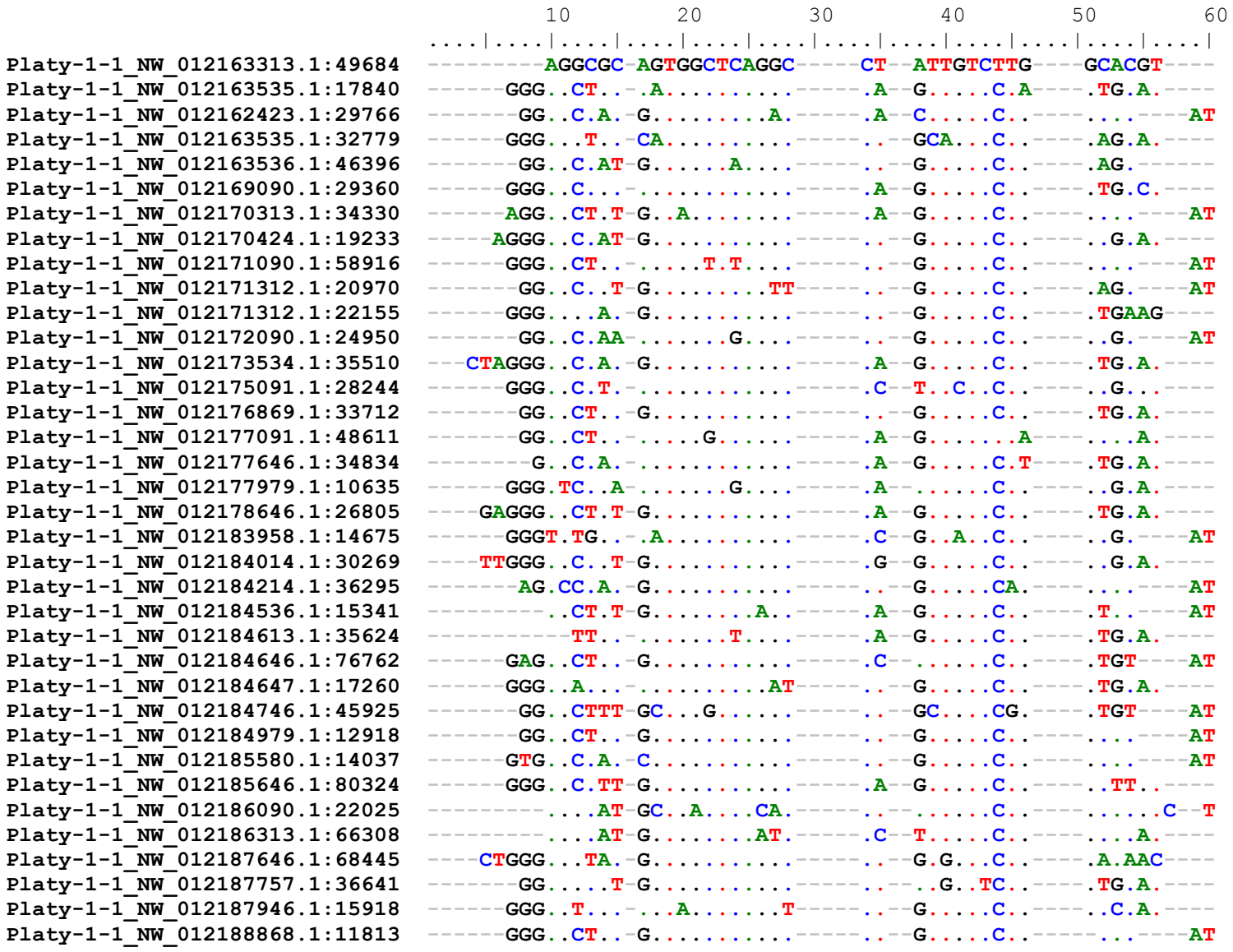
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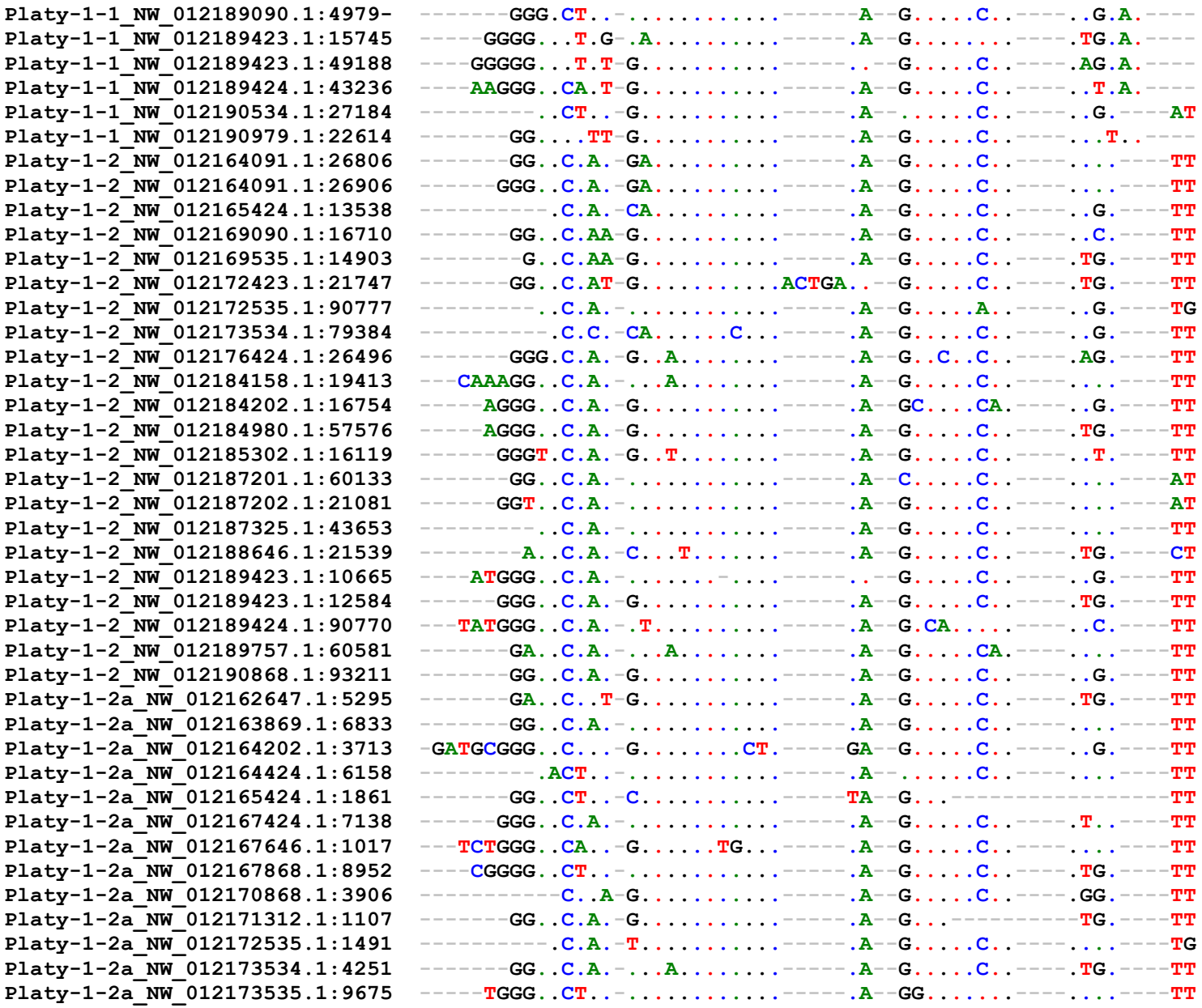
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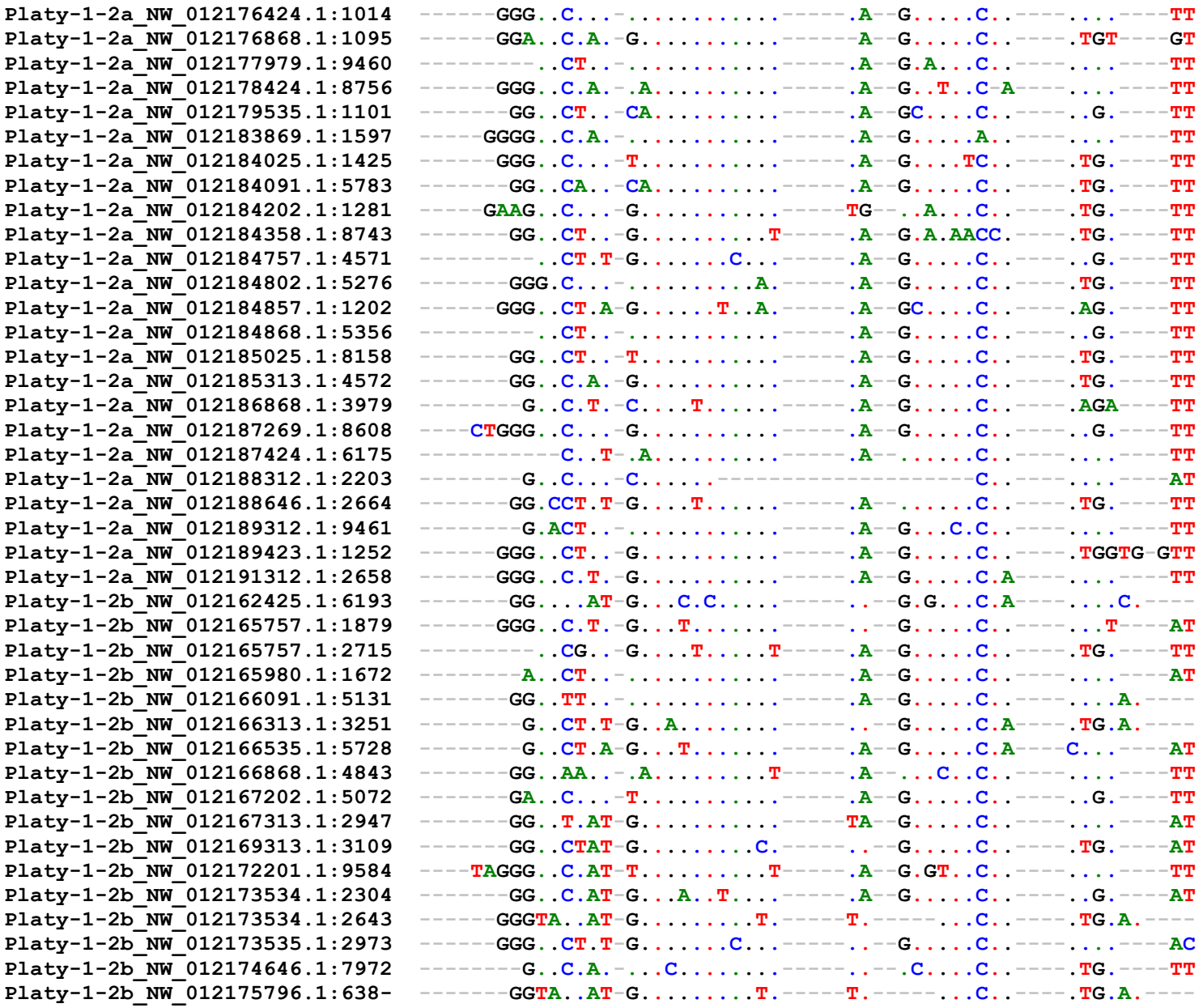
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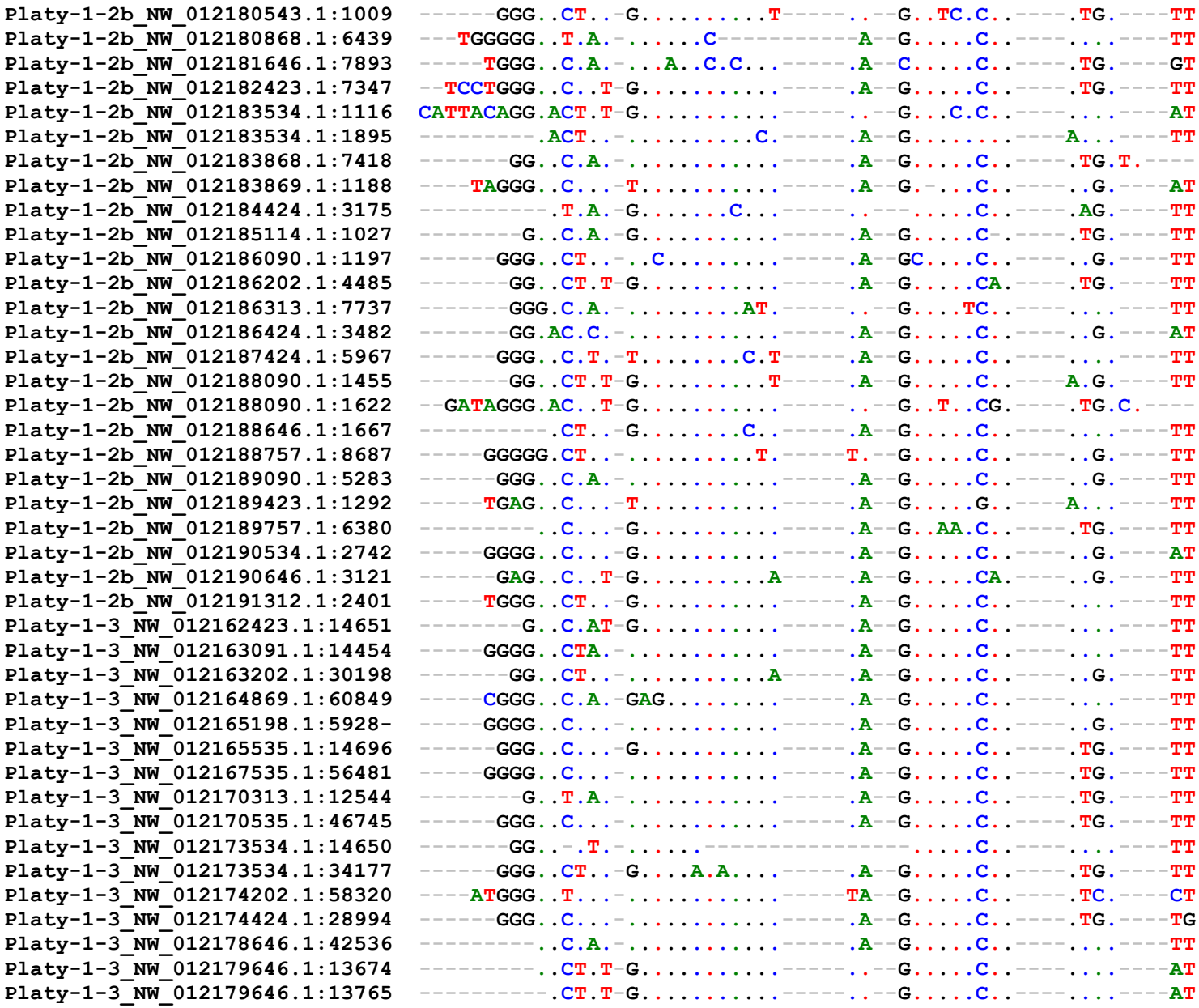
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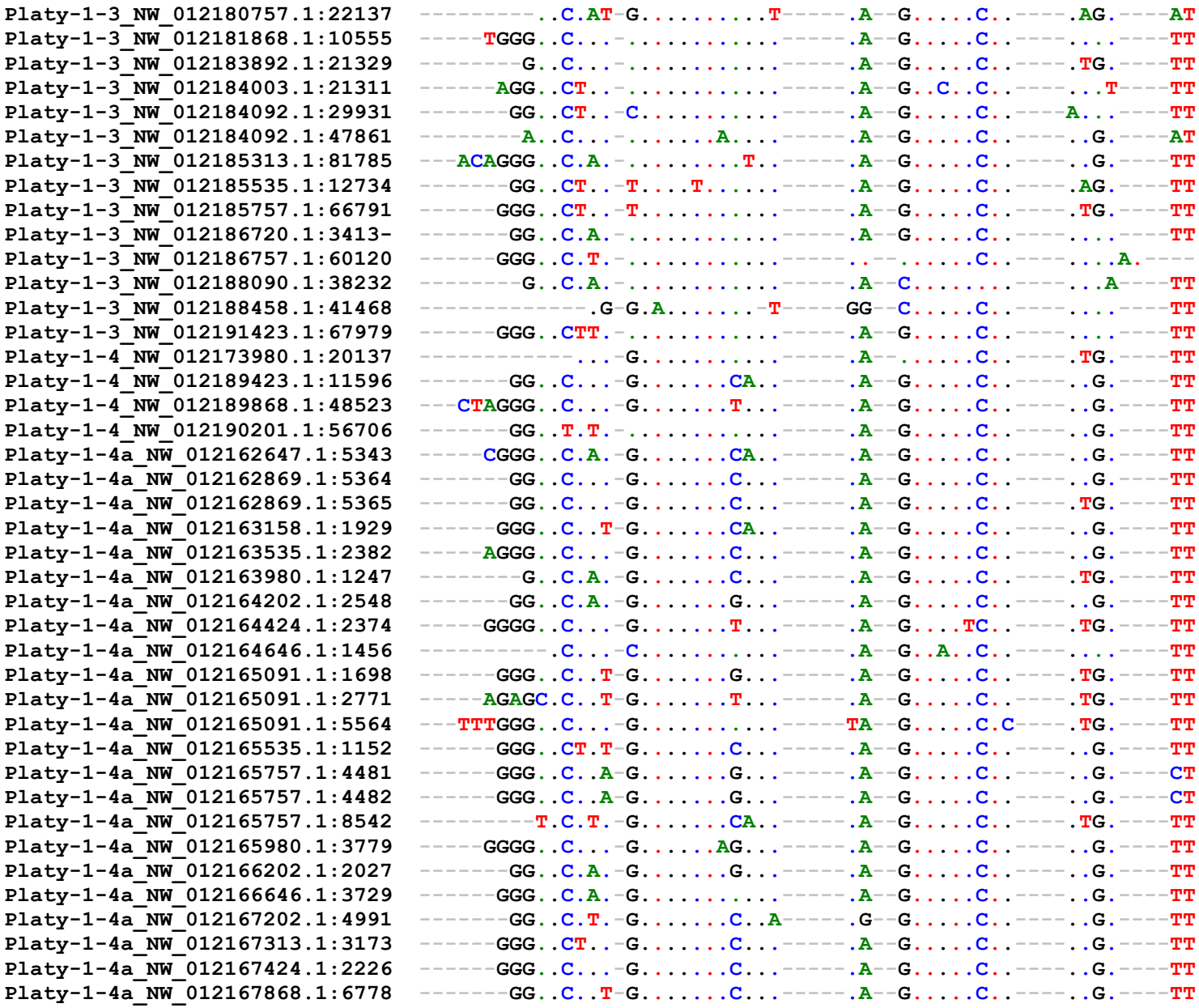
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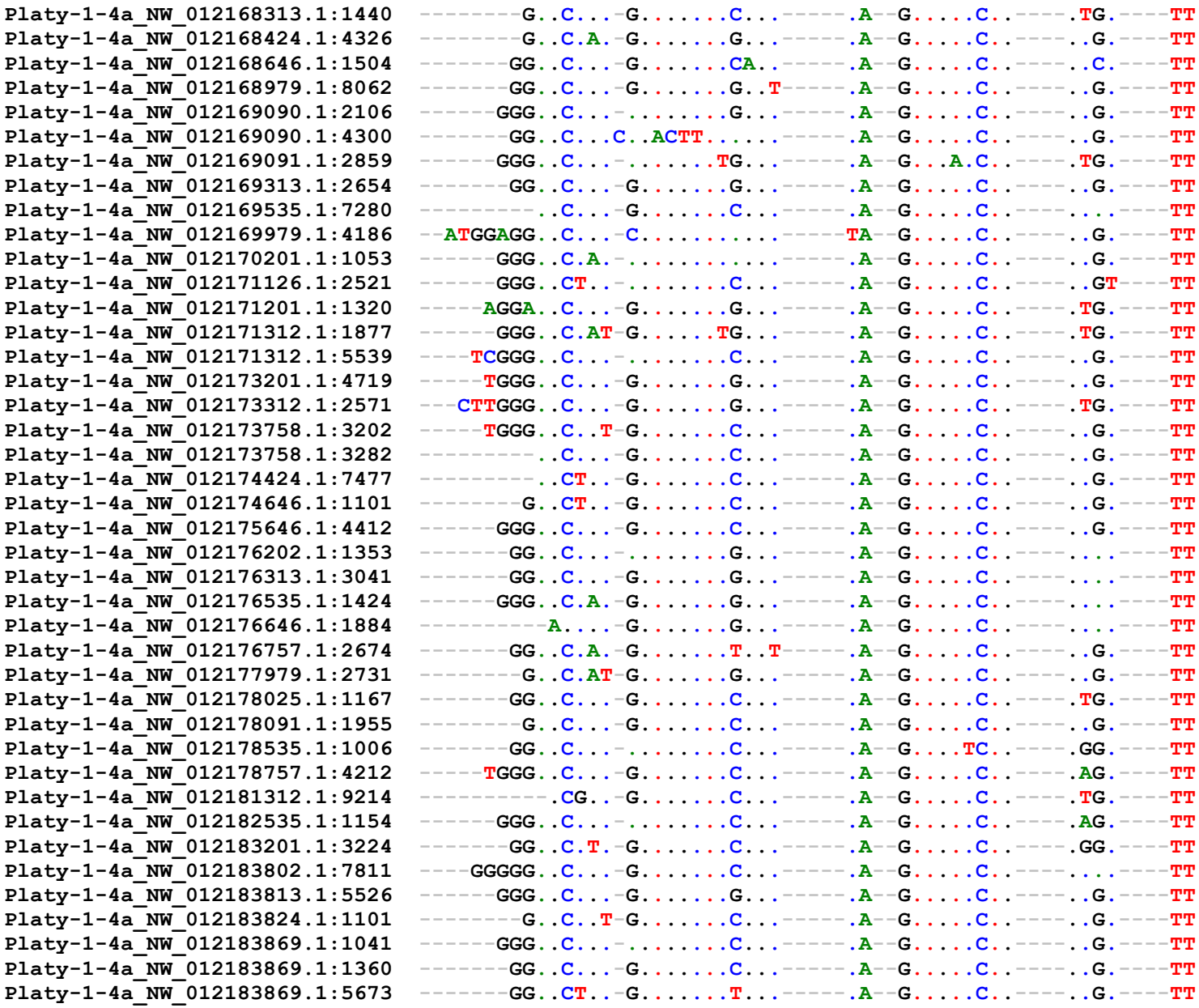
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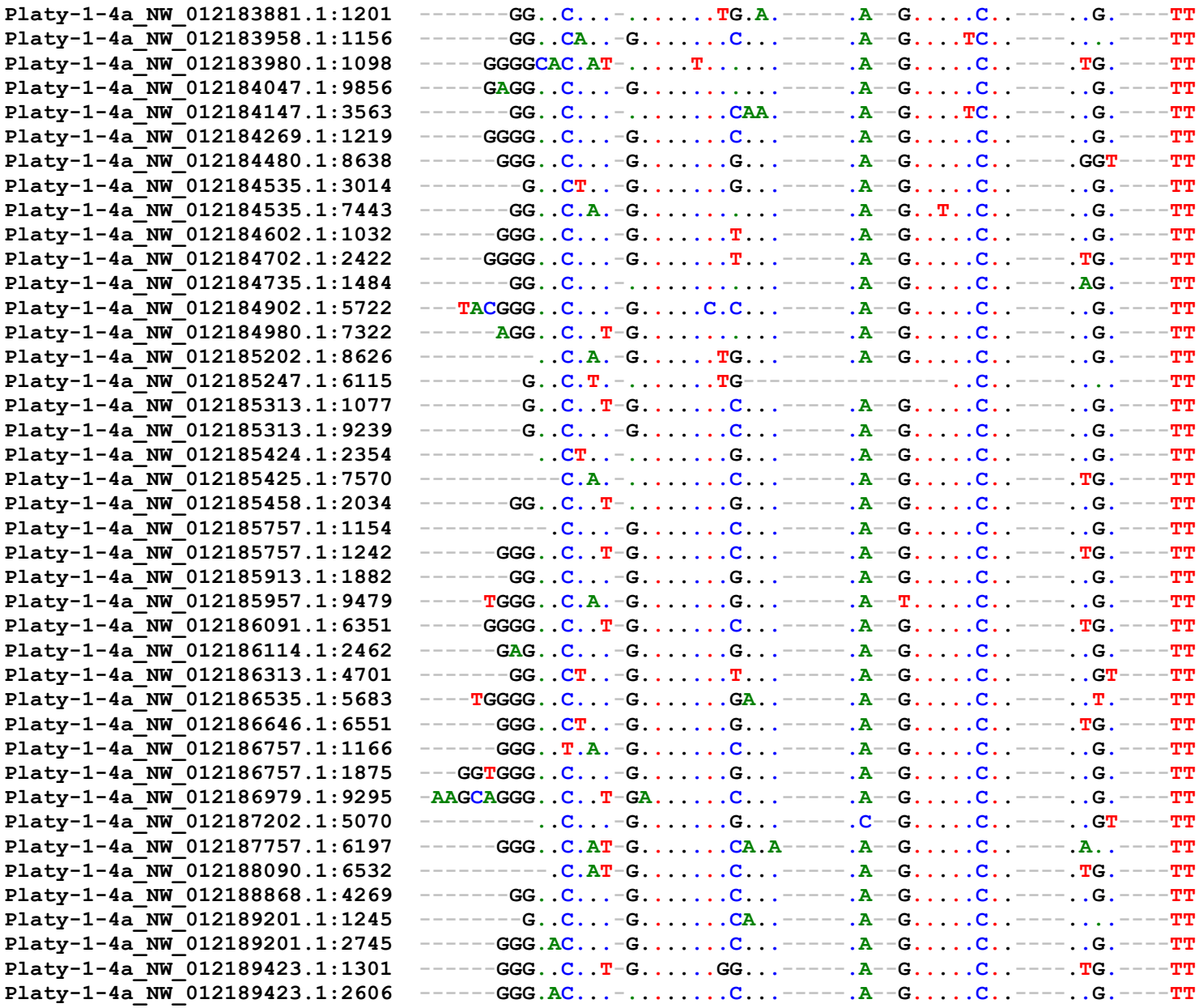
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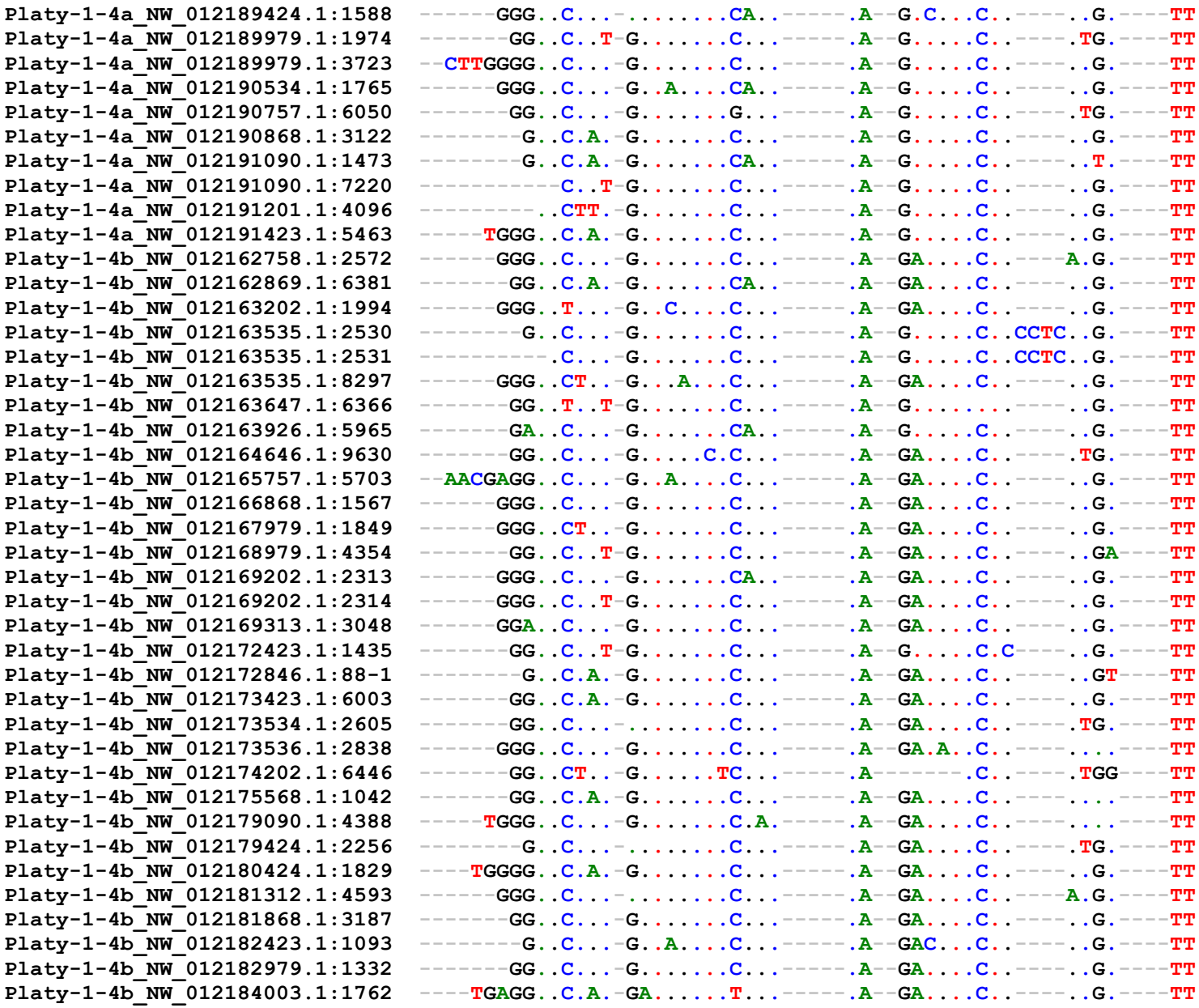
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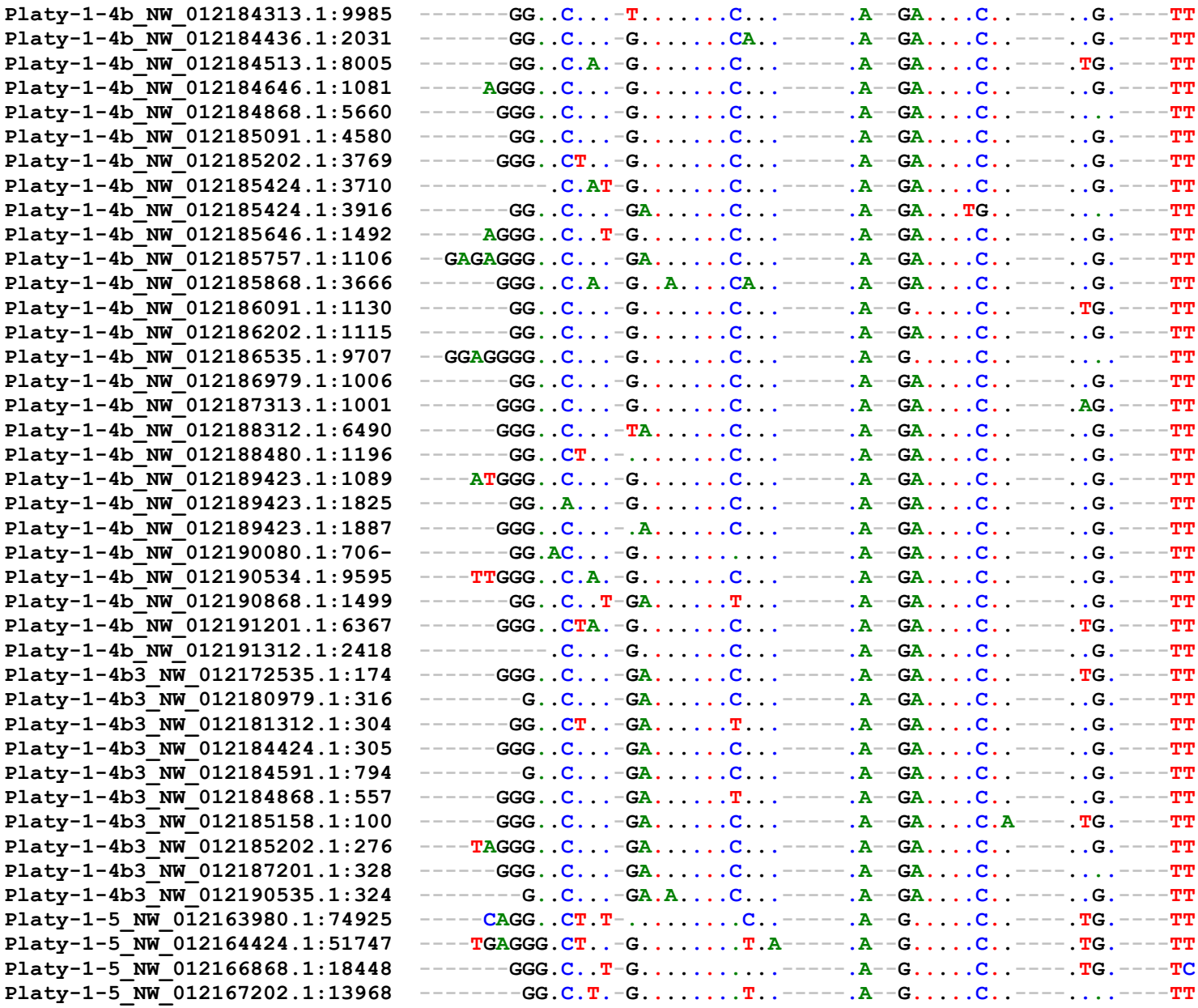
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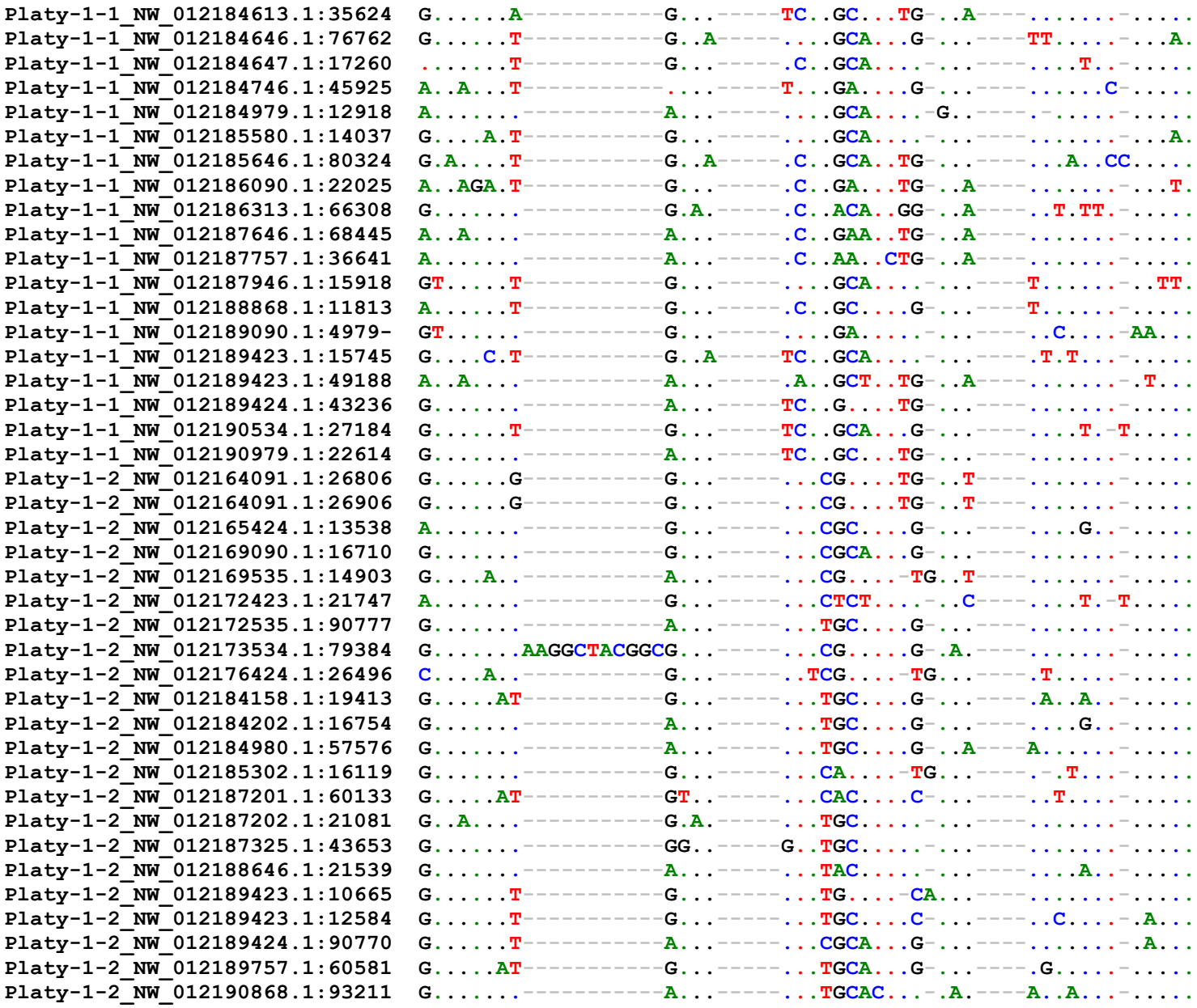
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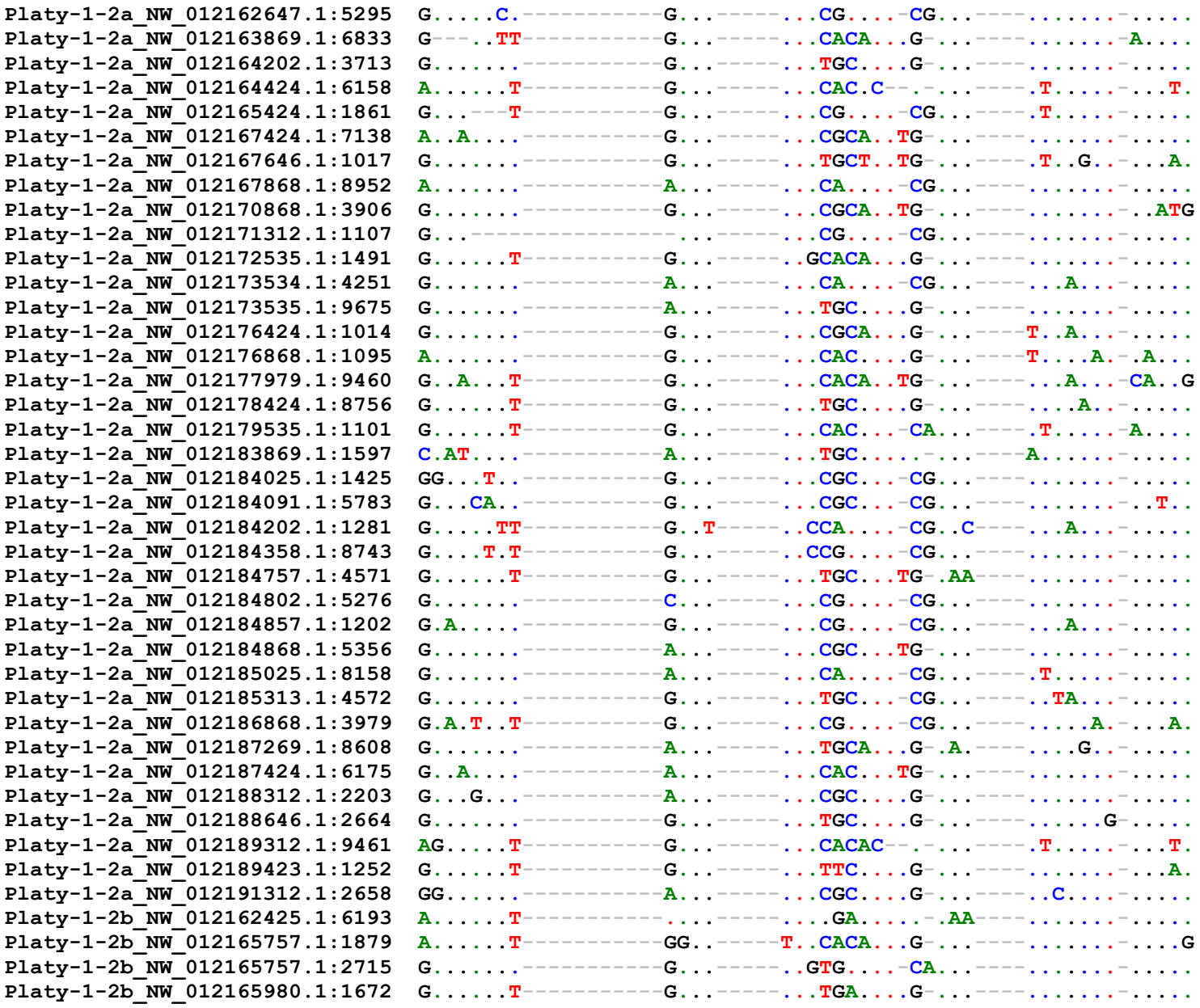
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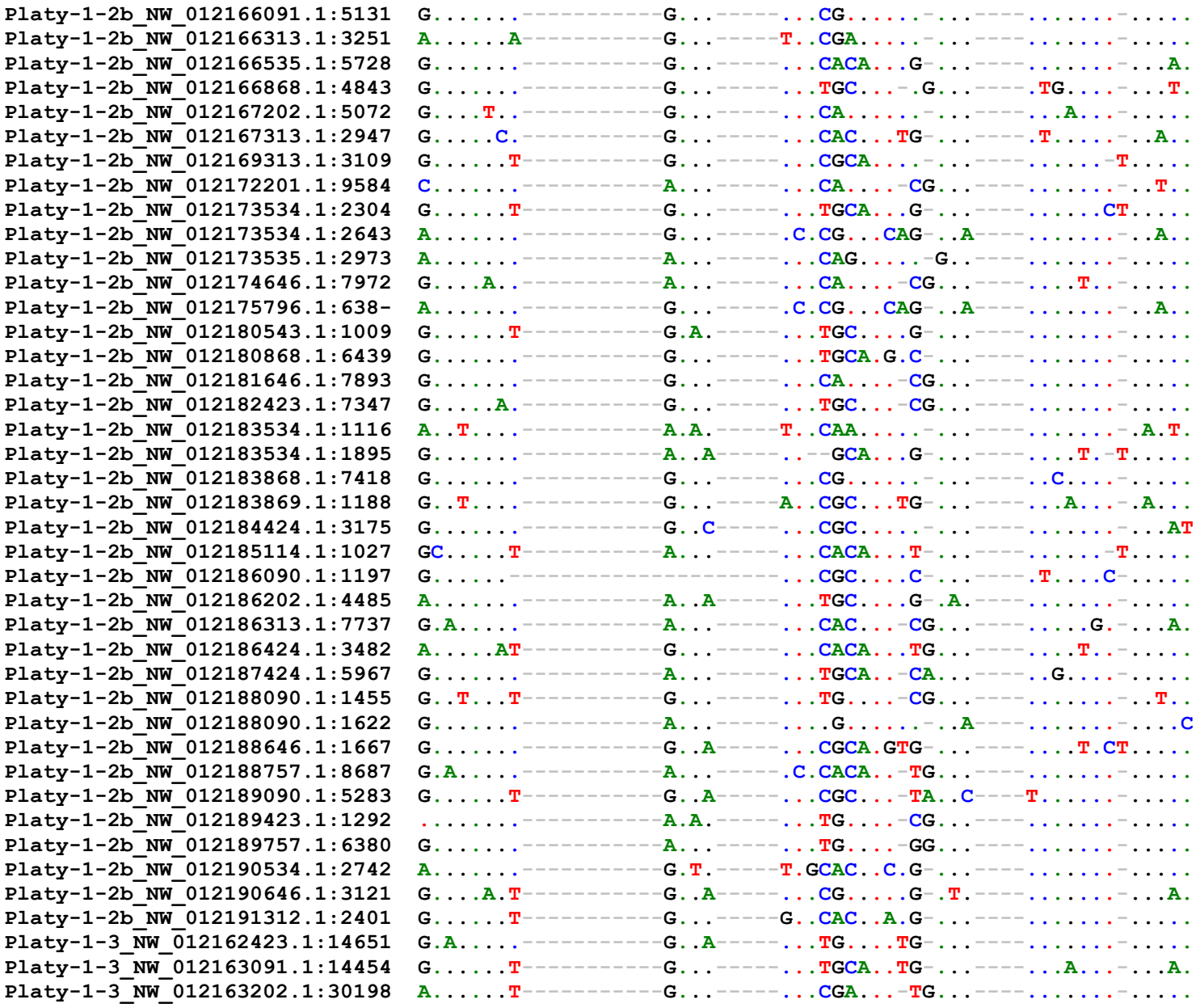
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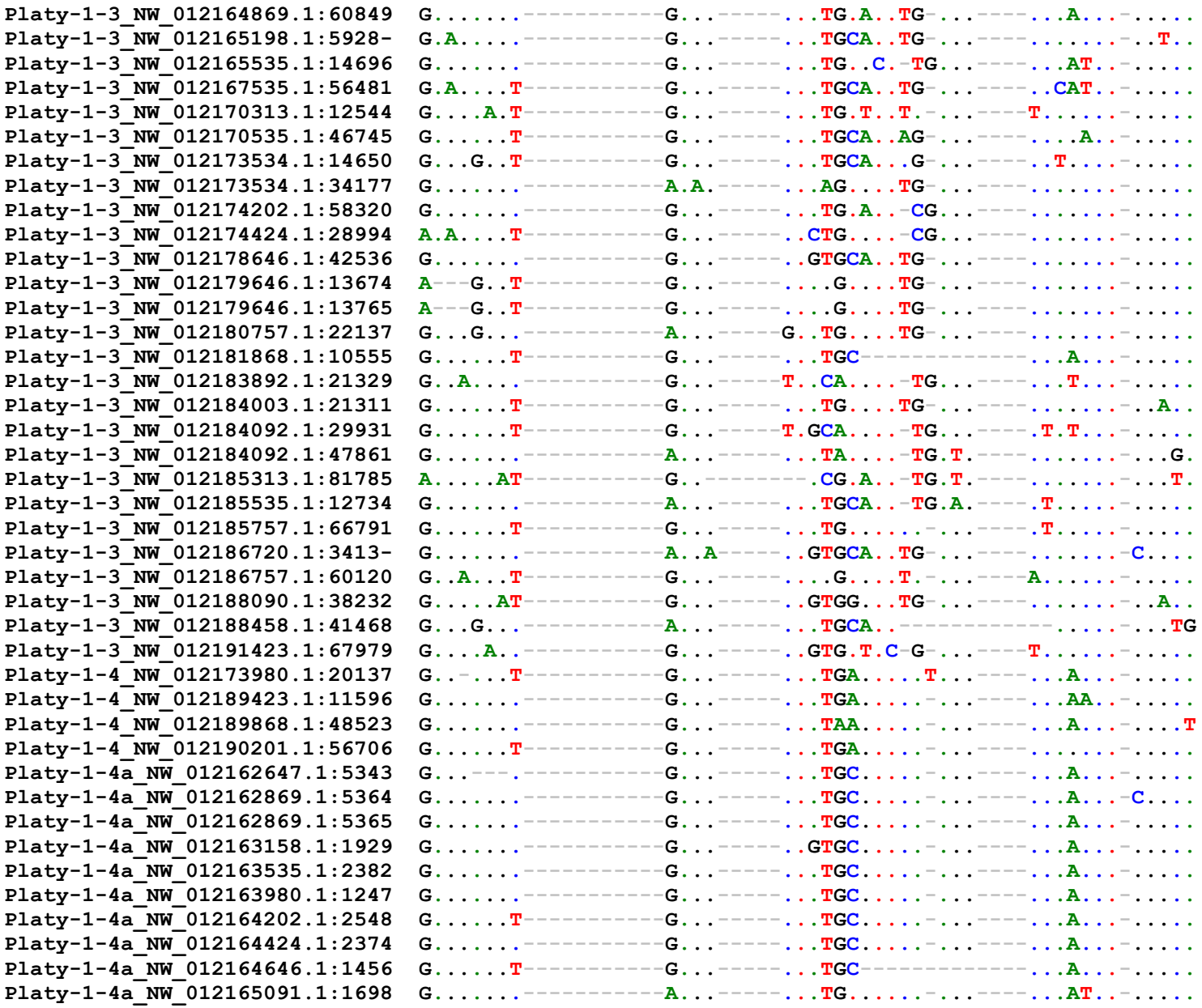
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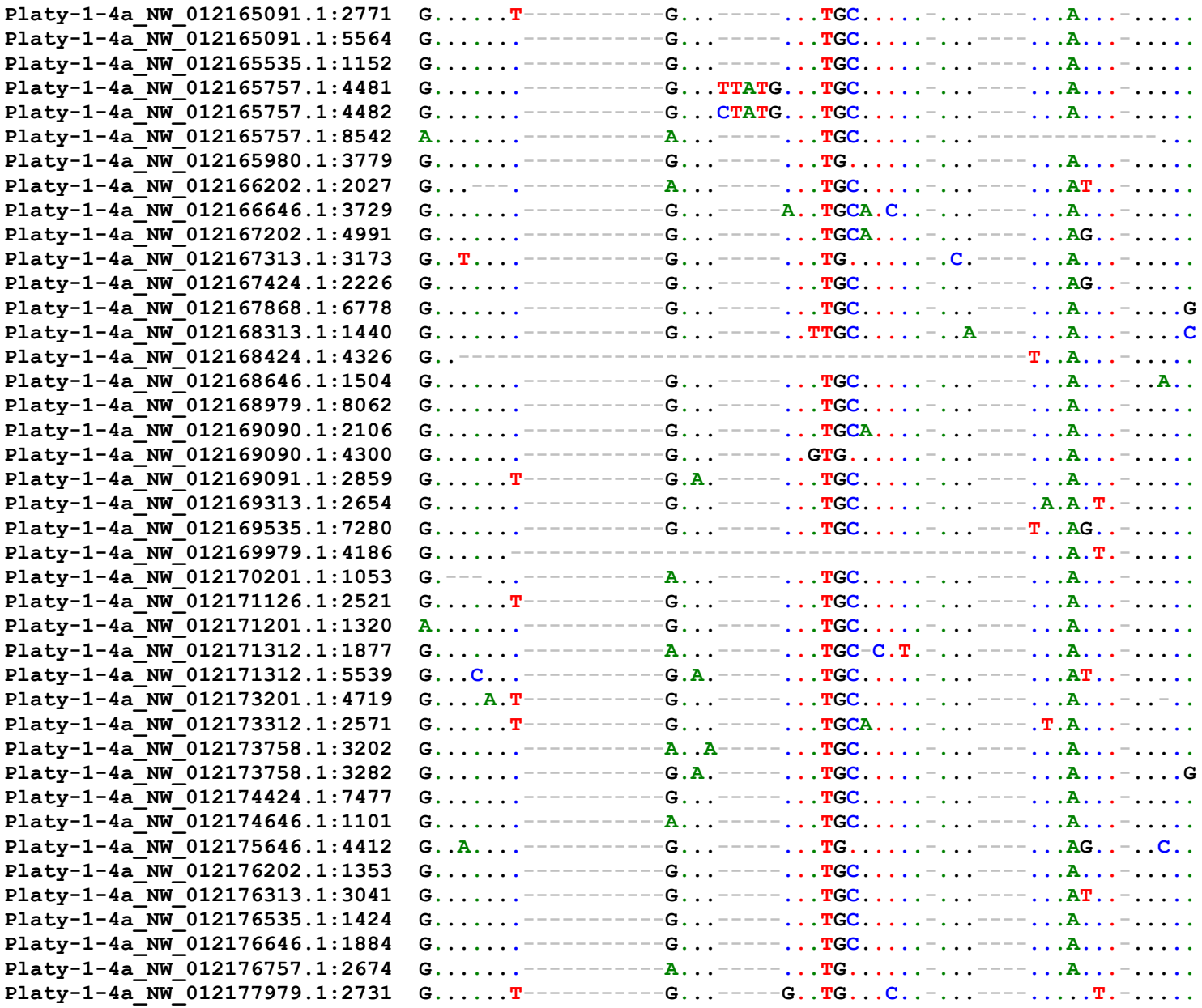
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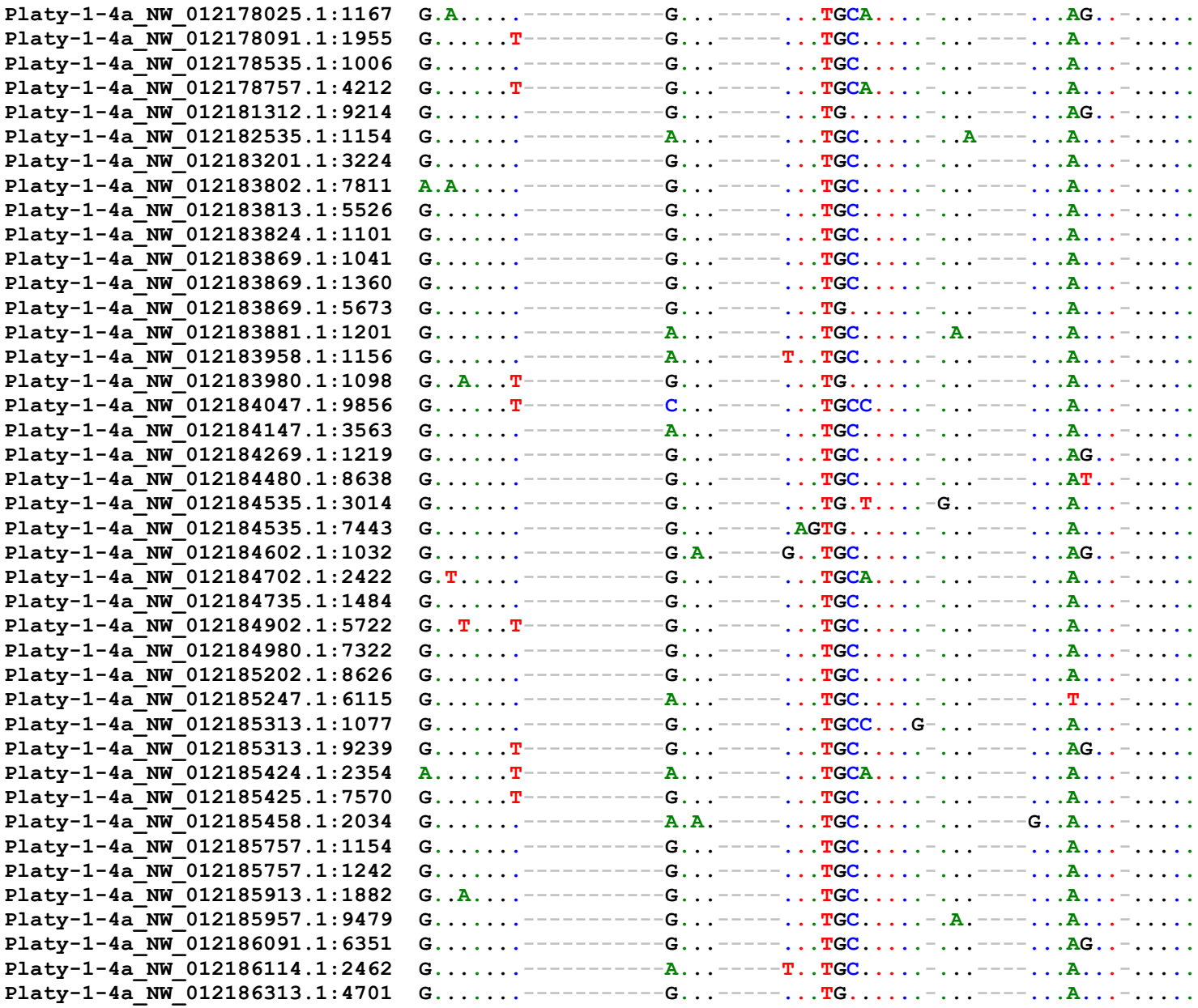
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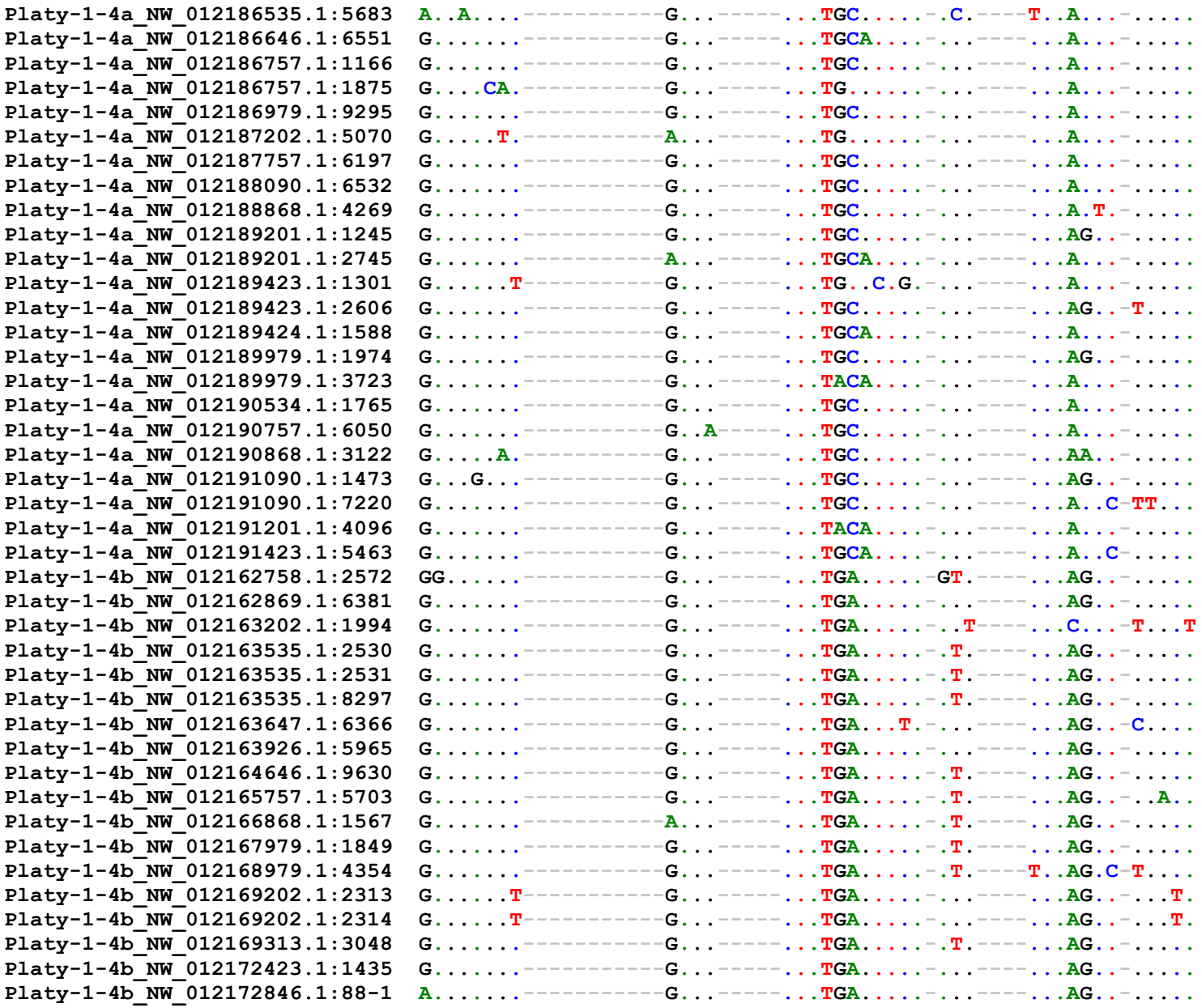
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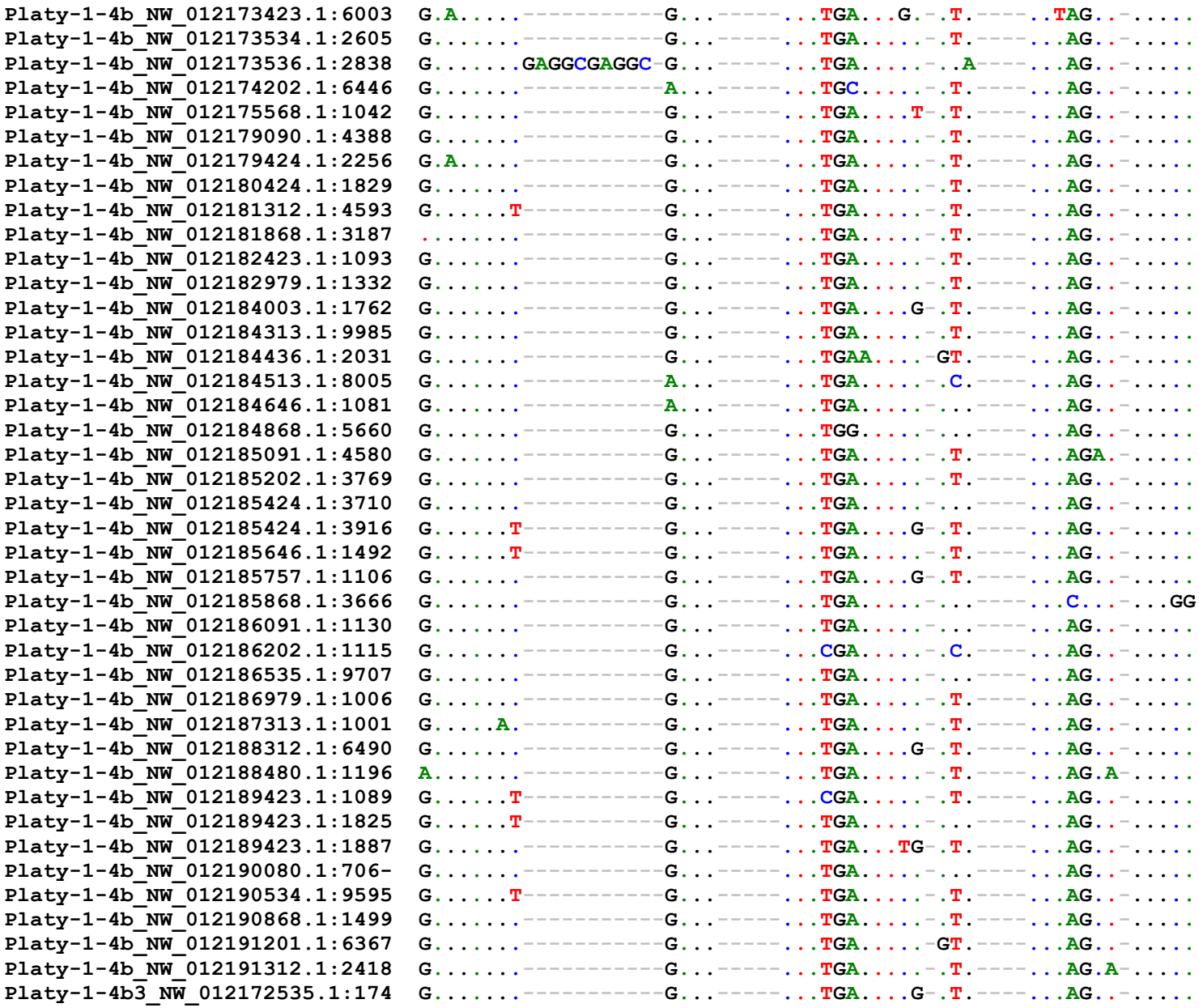
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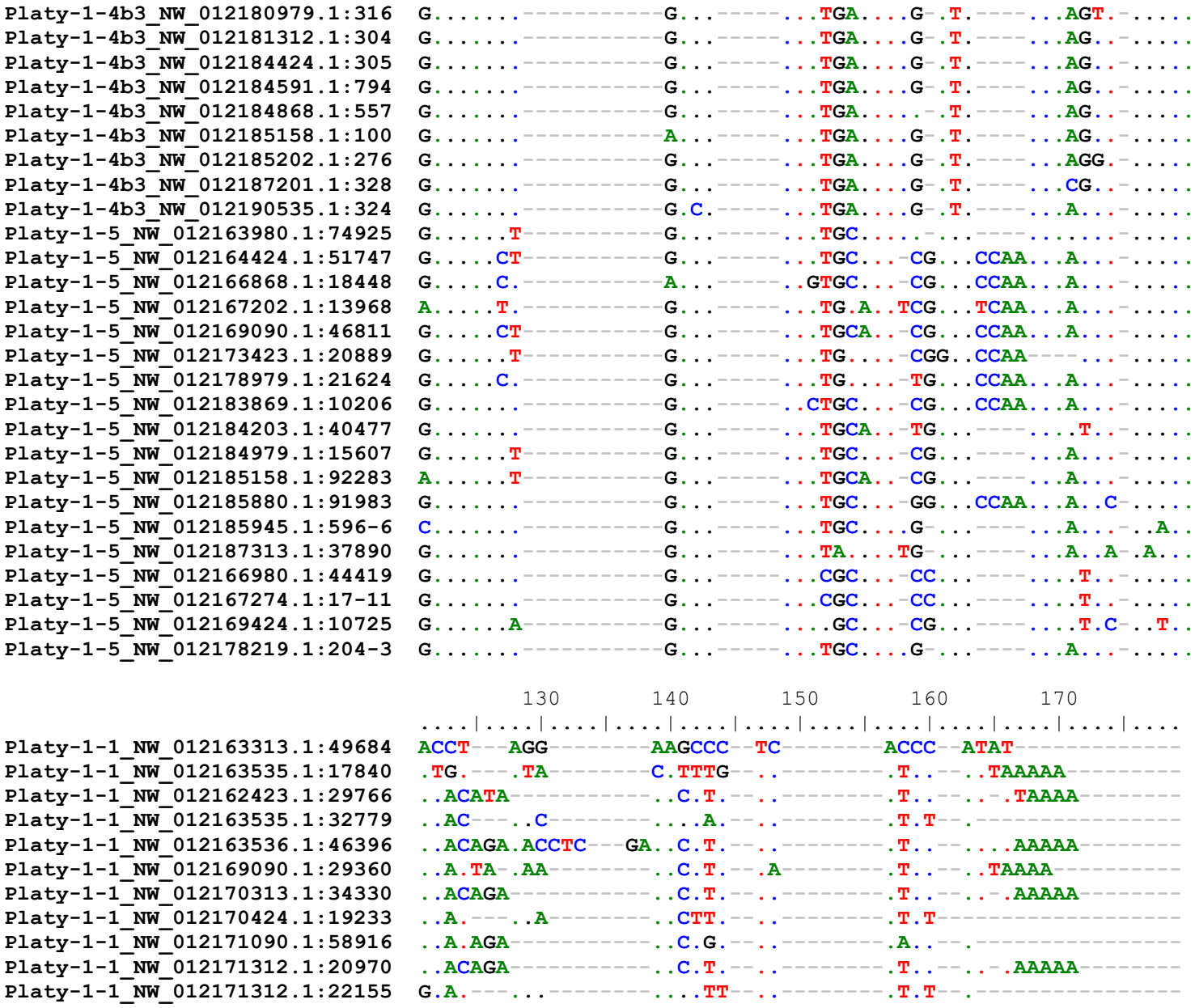
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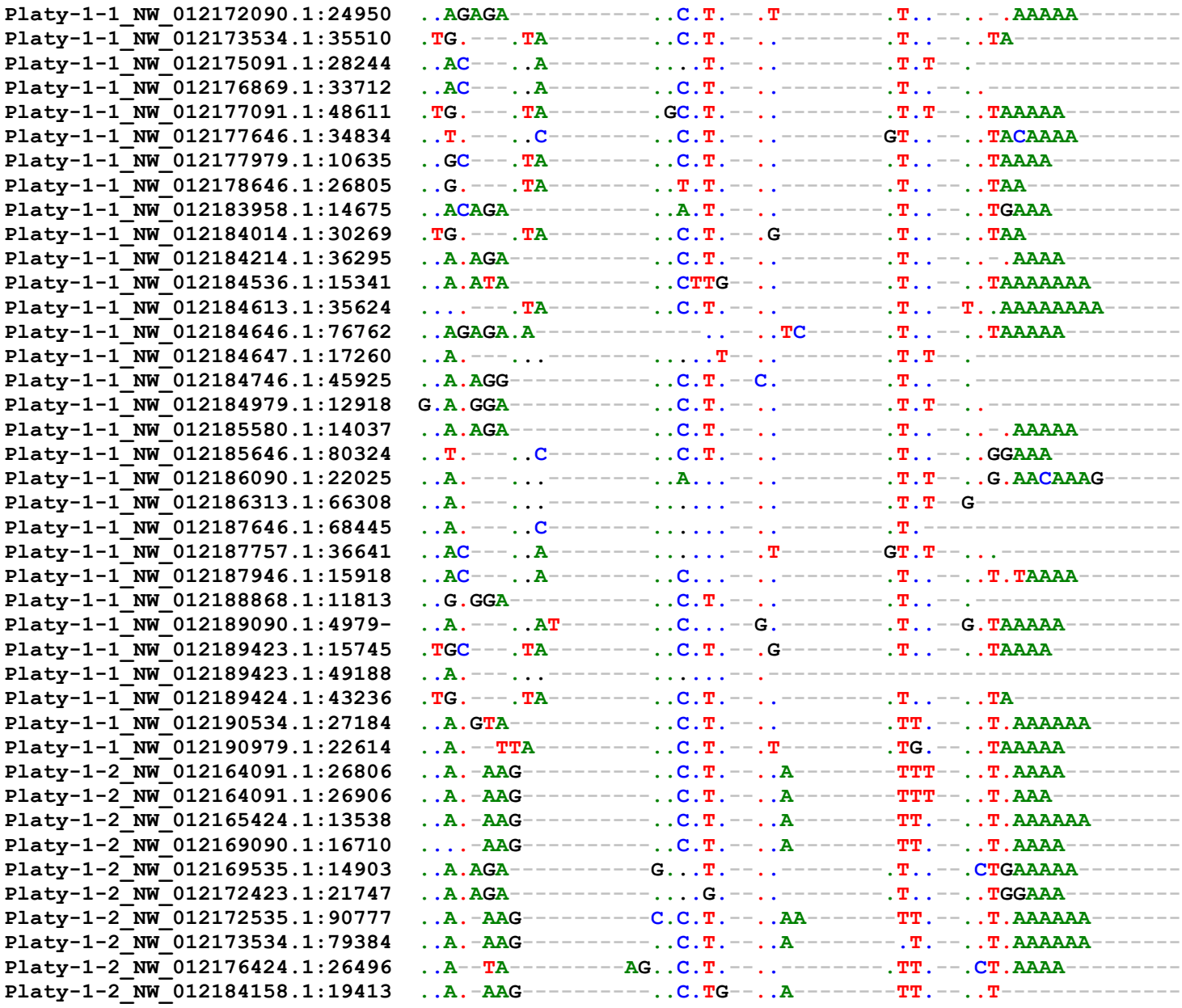
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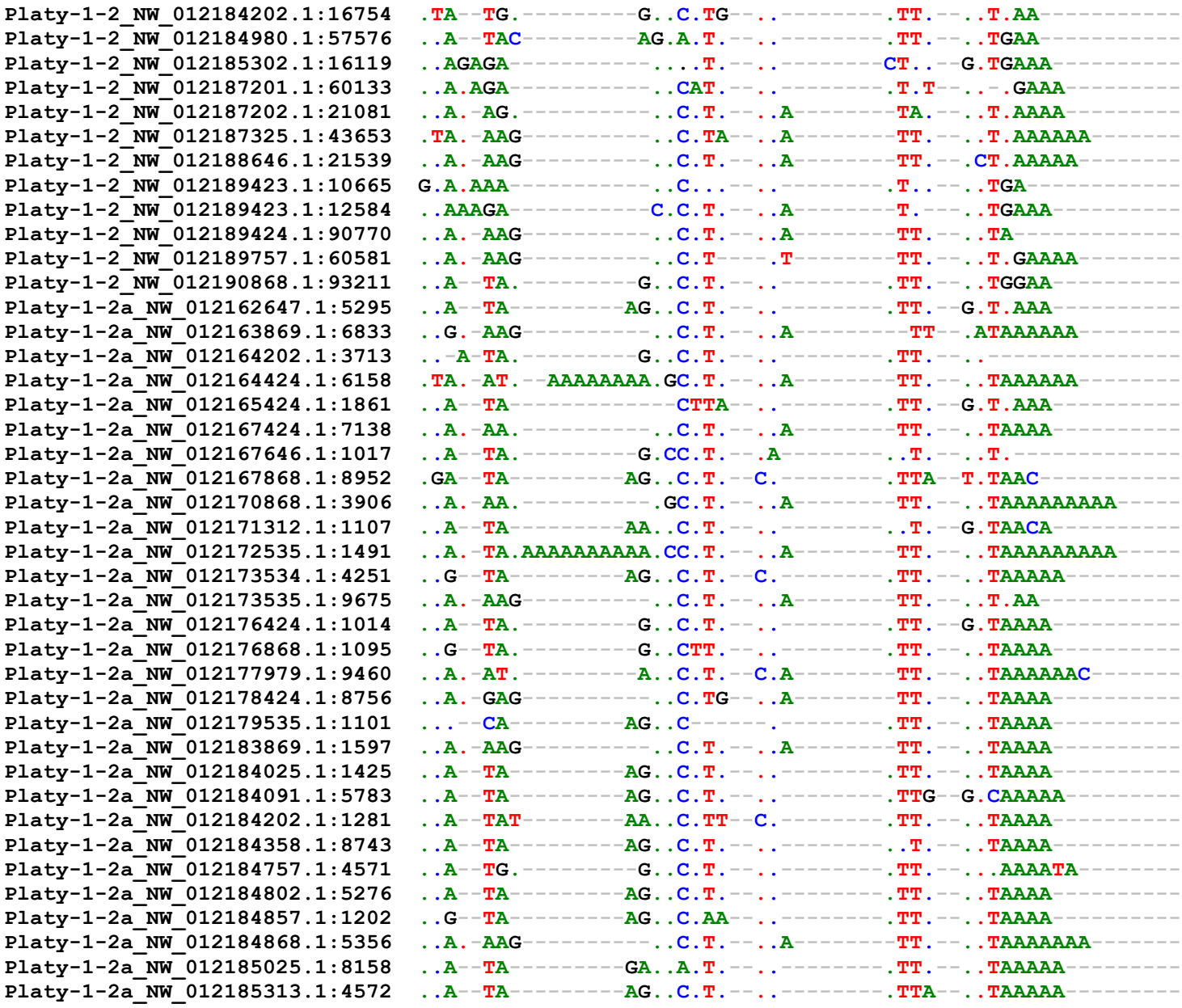
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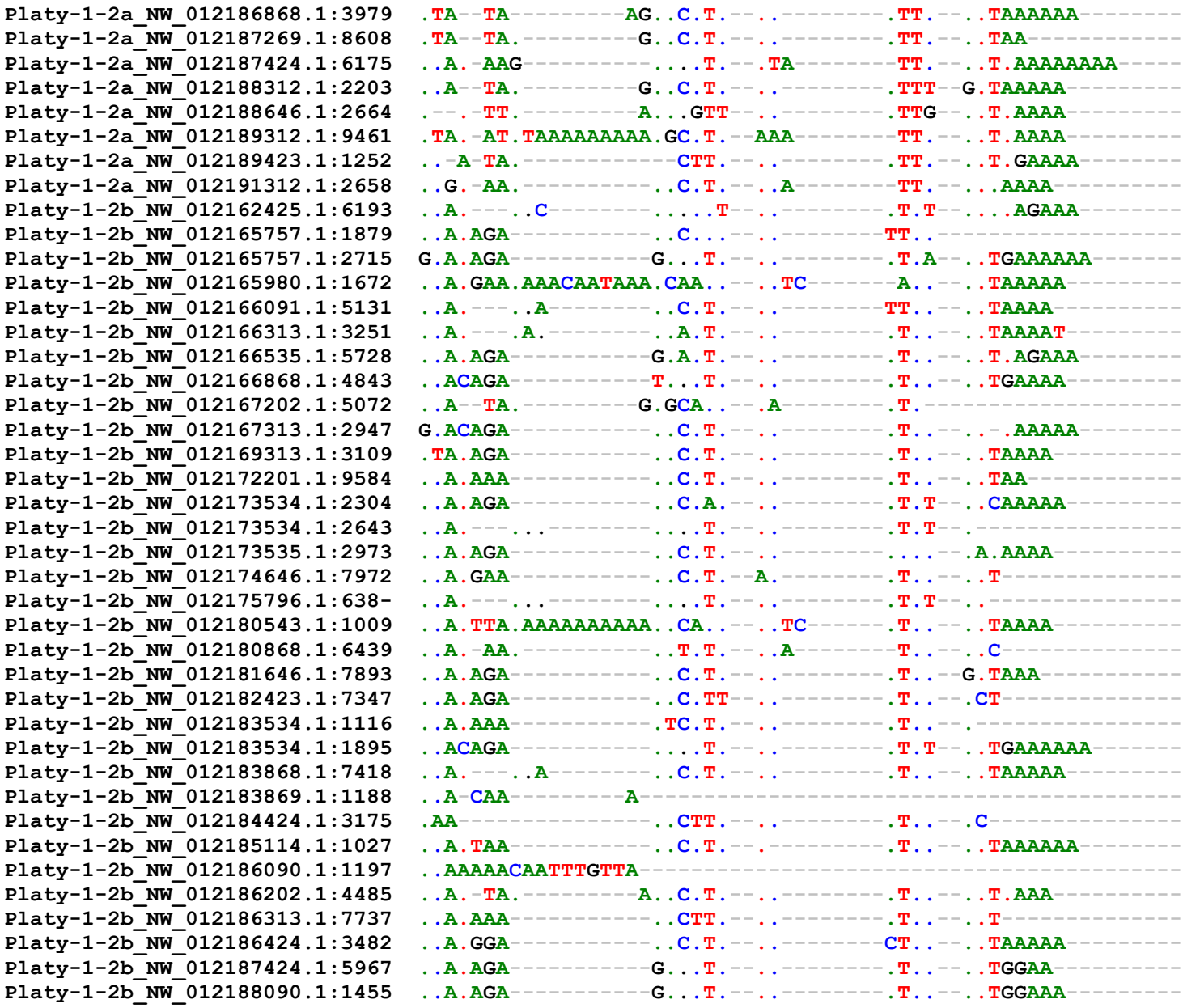
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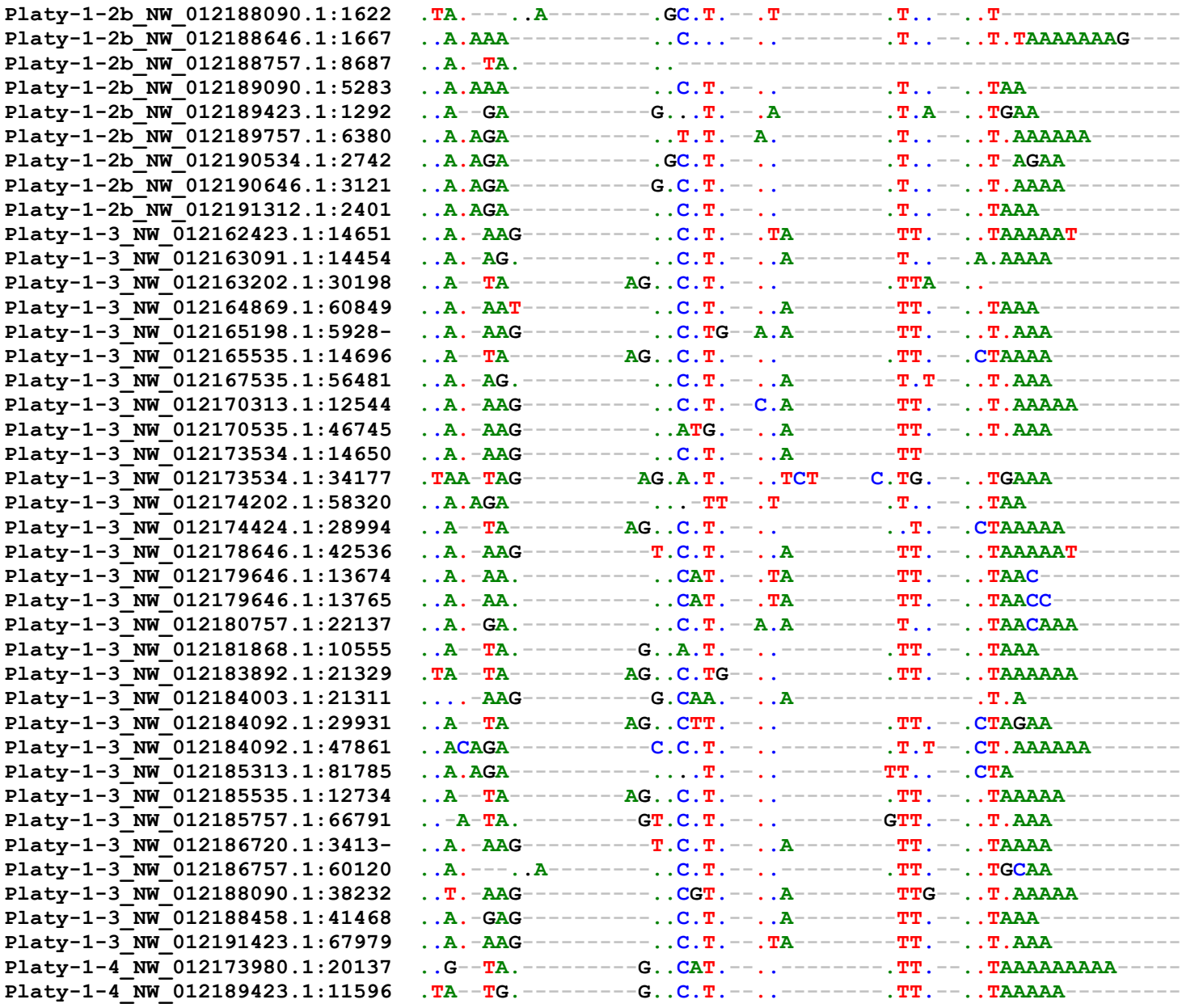
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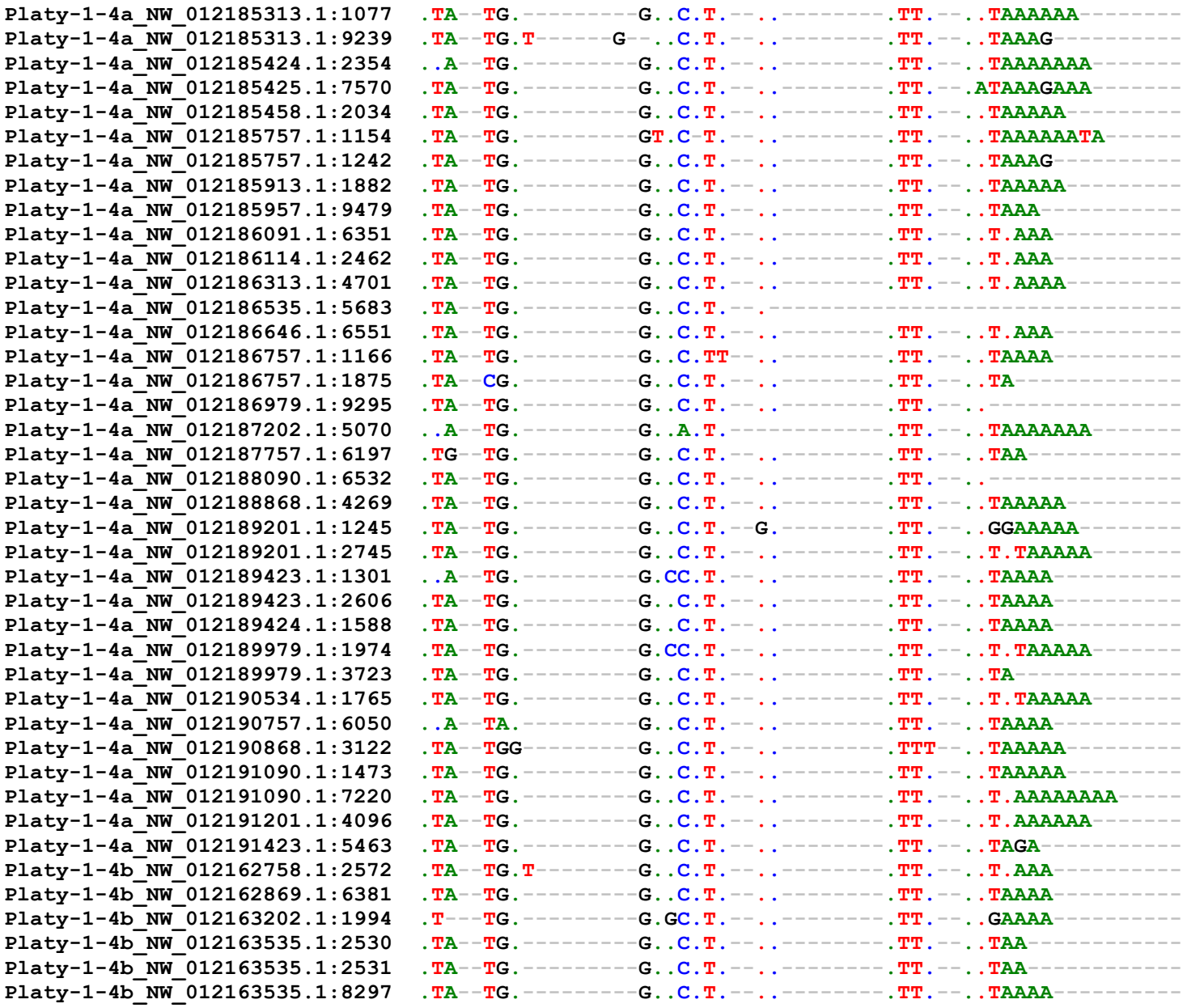
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Platy-1-4a_NW_012187757.1:6197
Platy-1-4a_NW_012188090.1:6532
Platy-1-4a_NW_012188868.1:4269
Platy-1-4a_NW_012189201.1:1245
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Platy-1-4a_NW_012189979.1:3723
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Platy-1-4a_NW_012190757.1:6050
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Platy-1-4a_NW_012191423.1:5463
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Platy-1-4b_NW_012163202.1:1994
Platy-1-4b_NW_012163535.1:2530
Platy-1-4b_NW_012163535.1:2531
Platy-1-4b_NW_012163535.1:8297

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Platy-1-4b_NW_012166868.1:1567  .TA--TG.---------G..C.T.---..---------.TT.---..TGAAA----------
Platy-1-4b_NW_012167979.1:1849  .TA--TG.---------G..C.T.---..---------.TT.---..---------------
Platy-1-4b_NW_012168979.1:4354  .TA--TG.---------G..CTT.---..---------.TT.---..TGAAAA---------
Platy-1-4b_NW_012169202.1:2313  .TA--TG.---------G..C.T.---..---------.TT.---..TAAAA----------
Platy-1-4b_NW_012169202.1:2314  .TA--TG.---------G..C.T.---..---------.TT.---..TAAAA----------
Platy-1-4b_NW_012169313.1:3048  .TA--TG.---------G..C.T.---..---------.TA.---..TAAAA----------
Platy-1-4b_NW_012172423.1:1435  .TA--TG.---------G..C.T.---..---------.TT.---..TAAAAA---------
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Platy-1-4b_NW_012173423.1:6003  .TA--TG.T--------G..C.T.---.A---------.TT.---..TAAAAA---------
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Platy-1-4b_NW_012173536.1:2838  .TA--TG.---------G..C.T.---..---------.TT.---..T.AAA----------
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Platy-1-4b_NW_012175568.1:1042  .TA--TG.---------G..C.T.---..---------.TA.---..TAA------------
Platy-1-4b_NW_012179090.1:4388  .TA--TG.---------G..C.T.---..---------.TT.---..TAAA-----------
Platy-1-4b_NW_012179424.1:2256  .TA--TG.---------G..C.T.---..---------.TT.---.CTAAAAAA-------
Platy-1-4b_NW_012180424.1:1829  .TA--TG.---------G..C.T.---..---------.TT.---..TAAA-----------
Platy-1-4b_NW_012181312.1:4593  .TA--TG.---------G..C.T.---..---------.TT.---..T.AAA----------
Platy-1-4b_NW_012181868.1:3187  .TA--TG.---------G.CC.T.---..---------.TTA--.A.AAAAA---------
Platy-1-4b_NW_012182423.1:1093  .TA--TG.---------G..C.T.---..---------.TT.---..TGAAAAA-------
Platy-1-4b_NW_012182979.1:1332  .TA--TG.---------G..C.T.---..---------.TA.---..TAAAAA---------
Platy-1-4b_NW_012184003.1:1762  ..----G.---------G..C.T.---..---------.TT.---..TGAA-----------
Platy-1-4b_NW_012184313.1:9985  .TA--TG.---------G..C.T.---..---------.TT.---..T.AAAA---------
Platy-1-4b_NW_012184436.1:2031  .TA--TG.---------G..C.T.---..---------.TT.---..TGAAAA---------
Platy-1-4b_NW_012184513.1:8005  .TA--TG.---------G..C.T.---..---------.TA.---..TAAAAA---------
Platy-1-4b_NW_012184646.1:1081  .TA--TG.---------G..C.T.---..---------.TT.---..TAAA-----------
Platy-1-4b_NW_012184868.1:5660  .TA--TG.---------G..C.T.---..---------.TT.---..TAAAA----------
Platy-1-4b_NW_012185091.1:4580  .TA--TG.---------G..C.T.---..---------.TT.---..TGAAAA---------
Platy-1-4b_NW_012185202.1:3769  .TA--TG.---------G..C.T.---..---------.TA.---.---------------
Platy-1-4b_NW_012185424.1:3710  .TA--TG.---------G..C.T.---..---------.TT.---...AAAATAA------
Platy-1-4b_NW_012185424.1:3916  .TA--TG.---------G..C.T.---..---------.TT.---..TAAAAA---------
Platy-1-4b_NW_012185646.1:1492  .TA--TG.---------G..C.T.---..---------.TT.---..TGGA-----------
Platy-1-4b_NW_012185757.1:1106  .TA--TG.---------G..C.T.---..---------.TT.---..T------------
Platy-1-4b_NW_012185868.1:3666  .T---TG.---------G.CC.T.---..---------.TT.---..TAAAA----------
Platy-1-4b_NW_012186091.1:1130  .TA--TG.---------G..C.T.---..---------.TT.---.CTAAAAA---------
Platy-1-4b_NW_012186202.1:1115  .TA--TG.---------G..C.T.---..---------.TAT--..T.AAA----------
Platy-1-4b_NW_012186535.1:9707  .TA--TG.---------G..A.T.---..---------.TT.---..CA-------------
Platy-1-4b_NW_012186979.1:1006  .TA--TG.---------G..C.T.---..---------.TT.---..T------------
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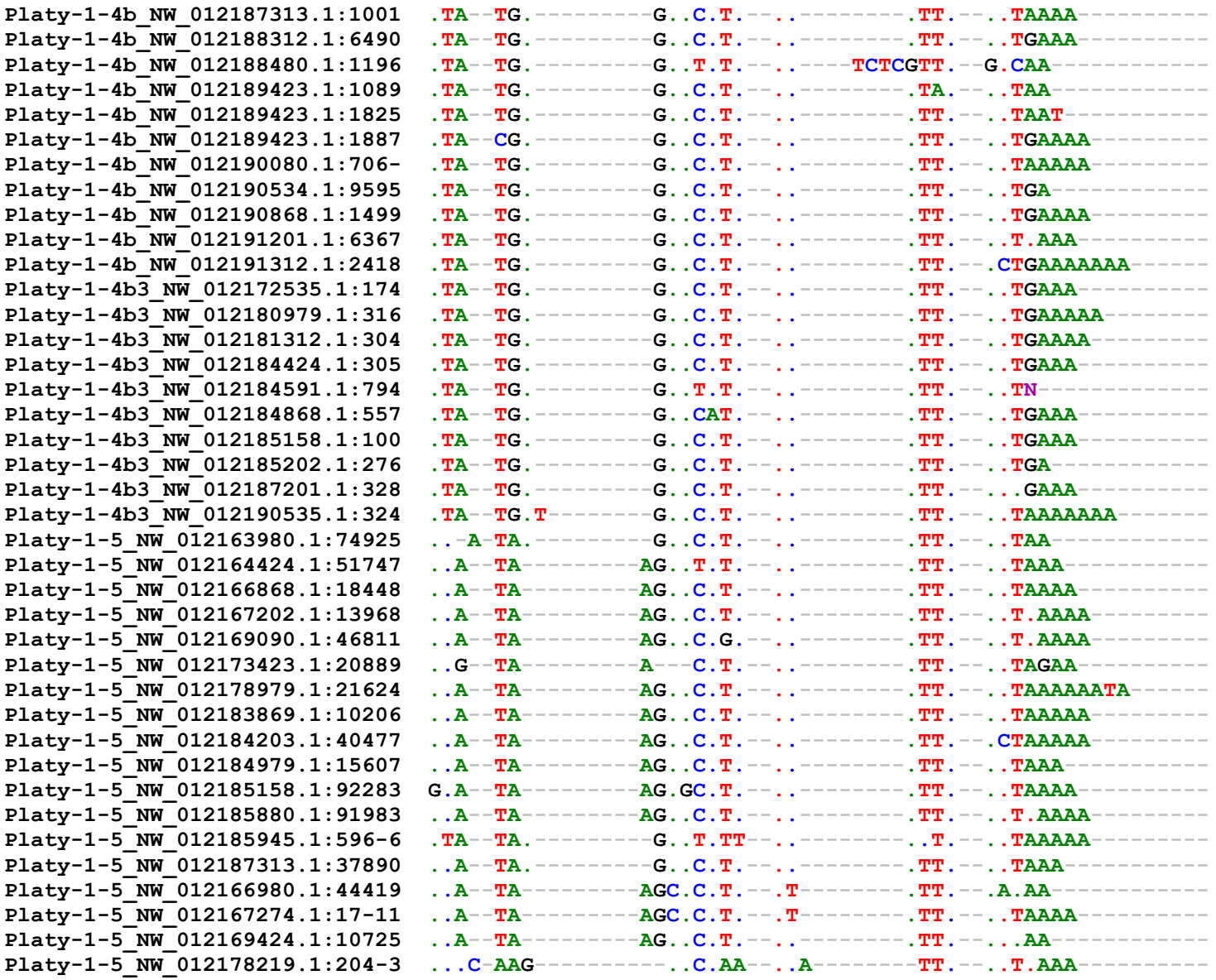
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Platy-1-4b_NW_012190534.1:9595
Platy-1-4b_NW_012190868.1:1499
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Platy-1-4b_NW_012191312.1:2418
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Platy-1-4b3_NW_012180979.1:316
Platy-1-4b3_NW_012181312.1:304
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Platy-1-4b3_NW_012184591.1:794
Platy-1-4b3_NW_012184868.1:557
Platy-1-4b3_NW_012185158.1:100
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Platy-1-4b3_NW_012187201.1:328
Platy-1-4b3_NW_012190535.1:324
Platy-1-5_NW_012163980.1:74925
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Platy-1-5_NW_012183869.1:10206
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Platy-1-5_NW_012167274.1:17-11
Platy-1-5_NW_012169424.1:10725
Platy-1-5_NW_012178219.1:204-3

Figure A2.1: Alignment of all full-length Platy-1 elements ascertained from the owl monkey genome. Dots represent a shared nucleotide while diagnostic substitutions are shown as the corrected base.

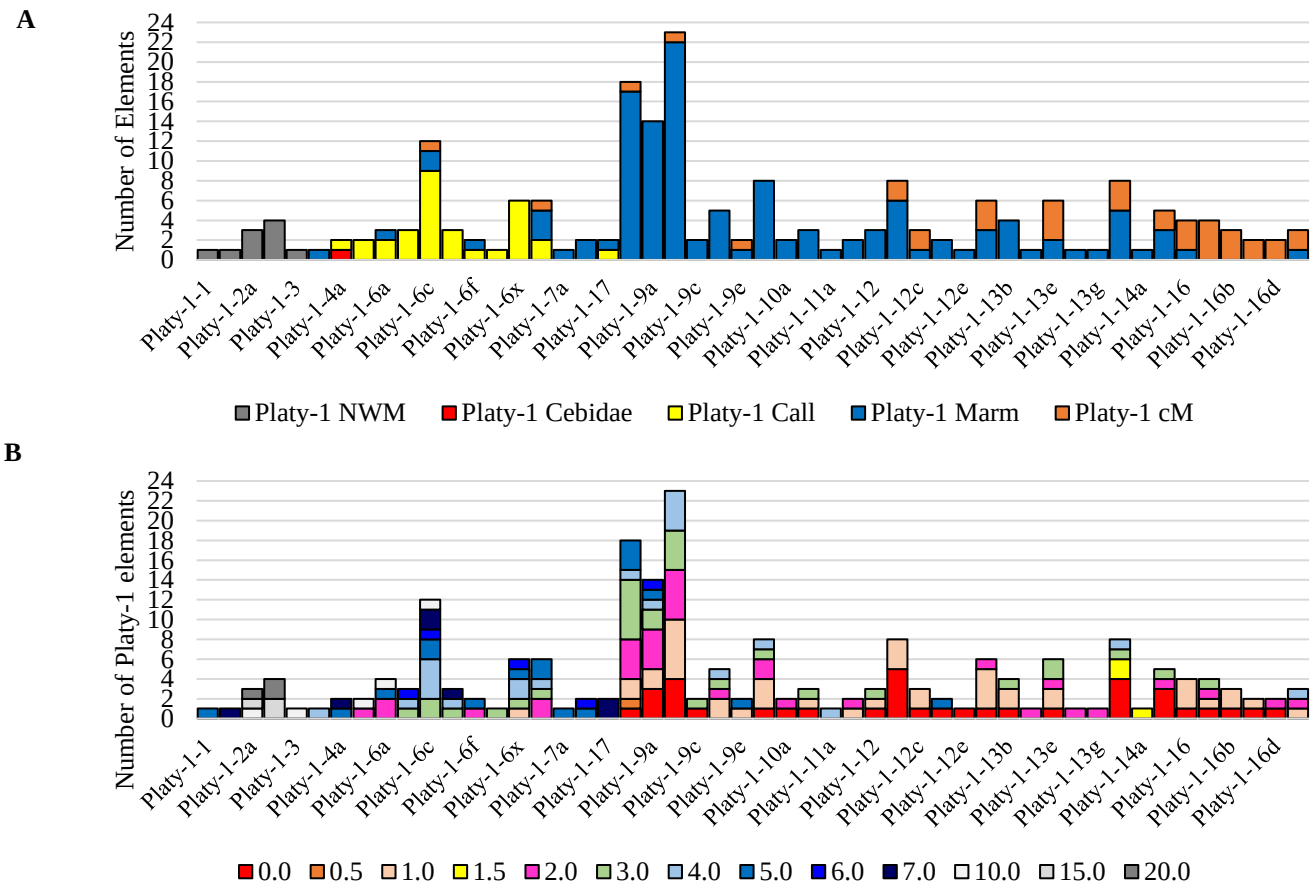

Figure A2.2. Platy-1 element subfamily distribution based on PCR. The data used to construct this figure is based on a subset of 204 Platy-1 elements reported in Konkel et al 2016. A) Platy-1 element distribution based on subfamily and lineage-specificity. Lineage specific insertions are defined as NWM: the element is homozygous present in all New World Monkeys analyzed (see methods in Konkel et al. 2016 for the DNA panel used); Cebidae: the element is shared in marmosets, tamarin, cebus, squirrel and owl monkey, while absent from other NWM; Call: the element is shared in Callithrichinae (marmosets and tamarins); Marm: the element is shared in pygmy and common marmoset while absent from other NWM; cM: the element is lineage specific to common marmoset. B) Percent divergence distribution among and within the Platy-1 subfamilies. The lowest percent divergence is shown in red (0.0) and the highest percent divergence is shown in dark grey (20.0)

Chapter 3

Table A3.1: SRA Dataset 1 (DS1)

Organism	*Cebus capucinus imitator*	*Callithrix jacchus*	*Saimiri boliviensis*	*Aotus nancymaae*
BioSample	SAMN04274558	SAMN02744555	SAMN00672664	SAMN03121886
Link*	SRX1435931	SRX535326	SRX084785	SRX795829
orgID	35931	35326	84785	95829
Platform	HiSeq2000	HiSeq2000	HiSeq2000	HiSeq2000
SRR	3136940	1274964, 1274963	315557, 315554	1692994
Avg. read length	200	200	202	202
# PE reads	389835802	390638988	420093332	449389076
# SE reads	5158797	9672404	18875241	6994913
Genome size (bp)	2717703182	2914958544	2608588537	2861684817
Coverage	29.07	27.47	33.99	32.22

* https://www.ncbi.nlm.nih.gov/Traces/study/?acc= + cell value

Table A3.2: SRA Dataset 2 (DS2)

Organism	*Saimiri boliviensis*	*Aotus nancymaae*	*Cebus capuchinus imitator*	*Callithrix jacchus*
BioSample	SAMN00672664	SAMN04274559	SAMN03121886	SAMN02744556
Link*	SRP000293	SRP050519	SRP066279	SRP041711
orgID	srp000293	37795	569822	44556
Platofrm	Illumina HiSeq 2000	Illumina HiSeq 2500	Illumina HiSeq 2000	Illumina HiSeq 2000
Runs	21	9	12	4
Avg. read length	202	250	202	200
# PE reads	3976583680	5313068084	2344525944	716367318
# SE reads	235006631	145302032	22126747	11290633
Genome size (bp)	2608588537	2717703182	2861684817	2914958544
Coverage	326.13	502.11	167.06	49.93

* https://www.ncbi.nlm.nih.gov/Traces/study/?acc= + cell value

Table A3.3: Lineage-specific *Alu* owl monkey primers

Name	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')
Aotus_106_018486916_6408515	AGTGTGCATACTCTCCAATCC	GGTTGACCTGGTACTTTCCTTTG
Aotus_601_018490587_8853934	GAGAACTGGACCAATTGATCTCC	cTCCCAACAAAACTGTCAATGC
Aotus_622_018491217_447777	TGACTTACTCTGGCAGGTTCC	AGAAAGGAGGAGTGAGCTGTG
Aotus_710_018492092_1121428	GCAAAGGGGCCACTATTATCTG	GCCAGGcCTTAACTTAGTGTC
Aotus_779_018493257_12381808	GGCAATAGTAGCCCCtAAACC	CCTAGGTTGAAGGCAGAGAAATG
Aotus_848_018494005_2176062	CCATAGCCCgTGTTTCTTGAG	ACTCAGcGCTACTCAGTTCTC
Aotus_1115_018497016_2208352	CcCAGGCACAATACCCTTTAC	GCCCATCTTTCTGtACCAAGG
Aotus_1120_018497016_3680404	GACCTTGTGACCTTGGTAACC	CgCAACTTTTGGCCTAGAATG
Aotus_1418_018500140_3847331	TCCCTCCTCCAAAATGCAGAC	GGCAGTTCAGGGTGACAAAAG
Aotus_1741_018501792_4329775	CACAAAAGtCAAAGGCAGAGTG	GGCTGTTTGTGCTAATTTCCAG
Aotus_1742_018501792_4527848	AATGcGCTTGACTACACTGAC	TGGAAcGAATGTGGAAGTTGG
Aotus_1780_018501822_6340167	GTTCTTGGTGTCTGTCAGGTG	CCAACTGCAATGTCTCTTCCC
Aotus_1819_018502053_725910	TTTGGCTCTTCACTCATCCTG	ACCCTTCACATTCCAGAAAAGC
Aotus_1834_018502140_5016284	TCCCTCTCCTTGTATCGTGAG	AAGGCTTGTGGTTTGTCTAGC
Aotus_1898_018502359_4474051	GTGCCACTCGTTTAACCCTAC	TCAGATTTTAGGCTCCCCAAG
Aotus_2158_018503256_629155	GTTGTTTGTGCTTTGGGTGTC	GAGTTcGAGGATTGCAGTGAG
Aotus_2188_018503329_4567940	TTTGGGGAGAGaGAGGGATG	GACCAGCtCAAACCACAGAAG
Aotus_2315_018503519_6467094	ATCTGTTCCCCTCTGTGACTC	TCCATCCTGAAGTCCTTTGAG
Aotus_2540_018503925_28655695	TGGCGATGTAAGAGCAAGTAAG	AGTGGTGGGTTAGGACTCTTG
Aotus_2730_018504720_1881871	CACCCAAGACACACCTATGAAG	CCGAGAAGTCACAAACAGGTC
Aotus_2779_018505187_2715950	GCAGAACCACCTCAACTCATAC	CACAATATGGGCTGCTACAAAC
Aotus_2845_018505315_2521430	gGAGGTAAAGTGGAAGGAATGG	ACCTTCACCATGACTGACTCC
Aotus_2897_018505596_1766745	GCTCAgCACACTTAGGTTTTC	CTTGGAAGATGCAGCAATTAGG
Aotus_3270_018506446_1374510	TAAGCAAATGGTGGCCTACTC	ACAGTTCACAAAGGGAGTAGG
Aotus_3581_018507789_8972613	AGGCCGTAAACACATTCCTTG	TGGTTaCCTTCCCAAGTGAATC
Aotus_3692_018508315_7887369	ATAGGGTCTTGCTCTGCTGTC	GGGAGTTAGGGGAAAGATTTGG
Aotus_3753_018508469_4764900	TCACAGTGTTGCATCTTGTACC	AGCCCTGAGTGAgTGGATTTC

Aotus_3842_018509268_1336944	gTGTGGACTTTGCAAACTTCAG	TCTcTGTGCCTTGAACATGTG
Aotus_3908_018509651_1897068	TGTAAGGGCTTGACTACTCAC	CAATTGCTcTTGTCTGTCTGG
Aotus_4545_018514661_3129113	AGGGGTTGGAATTCAGTGAAC	TCAGTTTTGGGTCGTTGGTTG
Aotus_4606_018486447_3972387	AGGACTTTGGAAATGGCAAGG	TAATGCCACTCCgTACCTCTC
Aotus_4878_018494243_1726229	CCCAGCTATCCTCAACTCAAG	TGCTCTGAACTAGGGTGATGG
Aotus_4920_018495964_125102	GGGAAGAAGCAGTAGGATGAC	AGAGACATCATCCAGGCTCTG
Aotus_4922_018495964_883361	CCAAgCCCTATCTGACTTTCC	TTCCAGgGTCATGGTGTAGAG
Aotus_4963_018497593_4989052	TCCCtTATTAAGTGCCTGTTGG	cTGGCTCAGTTCCCATCTTG
Aotus_5020_018499487_244936	AGACATCCTGACCCATCACAG	CTGACATTCTGCCAGCTTTTG
Aotus_5021_018499487_254620	AGATGCCCTTCTCAGTTCCAG	CTATGACACCTGCCCATTTCC
Aotus_5096_018500622_7185470	CCTGCgAGGTCTTTGTTATGG	GCTGCGATGAAGAaCTTTGTG
Aotus_5110_018501233_1458520	GCTTGGAGGTGCTGATTATGG	CCTGTCATGGATCTTGGTGAC
Aotus_5208_018501822_5213748	AGTGGGAGGGTTCATTCATCC	TTTCCCAGCCTGTTCTCTCTG
Aotus_5251_018502324_5286935	GTTCCATGAATGCCTGTTGATG	TGTGTGAGCTGAGTCCTTCTG
Aotus_5568_018505187_11856573	TCGAGAAACCTGTcTGTCCTG	TTCTCTGtGCTCAAGTCACTC
Aotus_5652_018505794_25448688	cGCAGGGAAGTTTTACCAGAG	GCACATTTTAcGGCGTTGTG
Aotus_5849_018507345_1374871	TTGGATGACAGCGTGACTATG	GTTTGGCCTCTGTCCTCATTG
Aotus_6052_018510022_1067711	TcGAGCATGATCAGTTACTTGG	CcGCTGCTTATGTCCCAATAG
Aotus_6140_018511496_468797	AACCTGATCCTGAGCCCTATG	GGTTCCAGGGTCTCAACATATG
Aotus_6206_018513365_2345920	TAACGTGGCAGTGACCCTTTG	CTTATGTTGGACTGGTGCGTATG
Aotus_6301_018503925_15522635	GTGATCCGGGAtATGACCTTG	AGGGTCAGTGAAACAAAAGGG
Aotus_6392_018501822_7473752	CCACTACACTCAGCCCATTC	TGTGTTCACTCCAAAGGTCTG
Aotus_6623_018494379_1182363	CAGGGAGGTGCAGCATAAATC	TCTTGACCTGGCTTTAACTGG
Aotus_6849_018503519_22322753	GTTGTTTCTCATGGGGAAGTAGG	GTGGTGCCTCAACTCTAATCC
Aotus_6855_018503546_7656090	CCTTCTTTCCAATCCCACCTC	CCAGGAGCCTTGGAATGAATAC
Aotus_6859_018503592_8739639	AGAGCCAGTTCTTACCAGGAG	GATGTAGTGGGCTCTTCAGTG
Aotus_7114_018508315_8516702	GAGTTCTGGGTACTTGACAAGG	CTGAGGTGGGCATAAGGAAAC
Aotus_148_018487315_12138096	GGGCTTCATATTCTCCTCTTGG	TGTGCACCCTATTCTGTAACTG
Aotus_347_018488552_4349452	TCTGGTTGTAGCAAGAGTGTG	GTATCCCACACCCTGAAACAG

Aotus_627_018491217_5502485	AACATGGGTGGCATTTATGGG	AGTTCCTTGACTGTCCCAATAG
Aotus_827_018493494_6605199	AACTGCTTCCTATGGACATCC	GCTGTGGAGTATGTCTGATGAG
Aotus_887_018494243_7511617	ACTCACAGGCAAGGTAAAATGG	tACTGTGAAGGGCTGCTTTTG
Aotus_1270_018499018_3640312	CTCATTCTGTgCAGCTCTGTG	CTGTGGGCATCTGGTATTGTG
Aotus_1345_018499555_9637688	TCCTGAACCCAATCGCTGTC	AAATCTTGCACCATCCCACTC
Aotus_1444_018500372_6746347	TGCTTCCTTTATTGGGGTTTGG	ATGCTGTCAGAGTTTCGAAGC
Aotus_1445_018500372_7246715	GAaGTTCTGAATCTgGGCTTCC	AGGTCCCAGAGATTGAAAAGC
Aotus_1446_018500372_7397646	ACCTTCCaTGGAGTTCTCAGG	AGTCATCTGGTCTGCTCAAGG
Aotus_1620_018501505_1280100	CCAGAGgAGCCAAAACTTCAG	CCAAAGGTCATCATGTCTTCCC
Aotus_1697_018501577_9448719	GAGGGCAATTGAGAAGCTGAC	GCTTTCtCCAATCCTCCTTCC
Aotus_1917_018502392_551286	TGGAGGTGGGAAGATGGATC	CCTTTTCAcTCTTgCCTCTCC
Aotus_2022_018502852_3895984	ATGACCCAGTTCAAGCCAATG	AGGATCTTGGAGTTGGATGGG
Aotus_2380_018503592_6421139	GTGCCAGCTTCCTCTCAAATG	CTAGCAGCCACGTTGTGTATC
Aotus_2402_018503629_1140417	TGCCCTTTCACCCTTAACAAG	TGGTCTCCCtCTGCaTATGTG
Aotus_2544_018503925_29434378	TTCCgTCCCAATTACCCAAAG	TTTGCCCCTCTTTGGTTTGAG
Aotus_3079_018505940_23366758	GATcTCCCACTCAGCTATTTAGG	TGCAAACCATCTATCCACCTTC
Aotus_3097_018505940_32345576	TGGTATCAgGCTGGTCTCTTC	AAACAGCTCAGGTCTGGTTTG
Aotus_3295_018506517_1391094	gTACCGAGTTCCACCTACAAAC	AGACATTTAGGGGAGAGAGGTC
Aotus_3424_018506919_3597178	ATCCCACACTCAGAaCCAGAC	AAGCTTTATGAGACgCCAGTG
Aotus_4339_018513070_1609795	TTTTgGGGCTTTTGGGGATG	TCCAAGGTGACAATGCCATAG
Aotus_4384_018513133_76378	GCCAGGGAACAGTCAGAAATC	CTTGTACCCAATTCCCAGTGAC
Aotus_4431_018513506_966214	CAAGCCCATTCCAGCAAGAG	GGCTCACTTCATTCTTCACTCC
Aotus_4486_018514082_7287702	AGCCCAAAATcGGTCTCATTG	GAGCGGGAATTAAGGTTGGAG
Aotus_4645_018487771_10691755	GGCATCTTCTTCAgTCATCTCAC	TTGCCTCAACTATGTGCCATC
Aotus_4723_018489399_20054653	AGGAGGAGGGAGGAAAAGAAG	GAAGACAGGATCCAAGCAATTG
Aotus_4735_018489399_5919141	CTGCcACCACATCCACATTG	CCAGGTCAGTTTCCACTTGTC
Aotus_4820_018491681_789269	CGTGAAGGTAGCgTGAAAACC	TTACCCAAAATGCCTGCAGTC
Aotus_5173_018501671_3165852	CCTGAAAGGGTAGTGTTGCTTC	GGGCCAACTGTAGAAGCATAAG
Aotus_5206_018501822_4711291	TGTGACAGAGTAGGTGCTTGG	CAGCCTGTGTGACTCAGTAAC

Aotus_5207_018501822_5131868	GGGTCCAATTCATAACTCACAC	TCAAGTTCAGATTCTCGCCAAC
Aotus_5306_018502852_3050795	GACCTGCCAAGATCACACAAG	TTTTCTGTTGGAGCACAGGAC
Aotus_5496_018503925_25360899	GTGGGGTGCAGGATGATTAAG	TAGCCCTAACCAAGcTGATCC
Aotus_5680_018505940_12024595	GCTTGGCTAATCTCTGGCTTAG	ATGCAGGCTTGGGTTTCTTTC
Aotus_5921_018508111_6319644	GTTTCCCCTGTAAGCACTGAG	CATCCTACATGTGgAGATAGACC
Aotus_5951_018508382_5659229	tAAAAGaAGCCTGGGGTGATG	ACAGAGACTCCCACATTGATG
Aotus_6317_018508453_838626	AGAGcGTTTGAGTCTCAGTTC	GCCATGTACAGCCCATTCATTC
Aotus_6335_018499555_5995878	GTCTAGCAAAGGTTTCGTATCCC	TCTTCGTACCTTCAAGCTTGTC
Aotus_6371_018494243_6223355	GGAATGTGGTGCTCATCTCTG	GGCCAATCACTGACAGACATG
Aotus_6430_018507789_443811	AGTTGGCTCTGAtTGGGTAGG	AAGGAAAAGATGGGGTGAAGC
Aotus_6604_018493257_3893871	GAAGtCTCAGTTGGGTGACAC	AACATGACTGCTCTCTAGTGG
Aotus_6633_018495559_735195	TCCAGGCTATAAGTGAGCTACG	CgAGAGTGCTGGAGTTACATG
Aotus_6637_018495601_188987	ATAAACATGTGGGCAGGGATG	TGCCAGATAAATCACAGCATGG
Aotus_6656_018496626_470991	TGGCTCATCAGGTCTCCAAAG	CGGAGGAAGCTCTTTGGAATAC
Aotus_6740_018501447_750287	AGGGCACTGTGAGTCTTCTTC	GCAATCTAGTCTGTGGCCAAG

Table A3.4: Lineage-specific *Alu* capuchin monkey primers

Name	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')
Cebus_60_016107316_17934820	GGACTACACATGCCAGATCTG	AACCACAAcCTTCCCTCTTTG
Cebus_66_016107316_3679973	AAGCTATGCACCAGACATGTG	GGGCTTGAGAAGAAAGAGTGG
Cebus_99_016107318_494442	TGAGTTGAGGGAAAGCCTTTG	TCACTTCATTAGCACACAAGGG
Cebus_218_016107325_3343127	CCAGCATAGTCTTGAACACCTG	AGCCTCAAGACACTGGACTTC
Cebus_286_016107328_6144398	CAGGCATCATTCCTGTCATCC	TGGCTGCAAATCTAGATCCAAC
Cebus_299_016107330_1103840	GGTGCCCAGATTGTAATAAAGC	GGGgCATGATGGTGTTTGAG
Cebus_314_016107331_3584373	GATGTGCAGATGGGGAAGATG	AGGCAAAGACTGTGATCATCC
Cebus_325_016107332_4137401	TCCAAACTGAAGCCAAATCCC	TACCACACCCATGCCCTAATC
Cebus_351_016107333_3271657	CTCTGGGGTTTGACAAGTGTG	TGCACACCTTGGTATTTTCCC
Cebus_360_016107333_7055183	AGAGGTGCATGACTGAGATCC	ATTCCCTCAGCTTCCCACTAC
Cebus_471_016107340_660428	TCAGTGTGCCAAGTACTATGC	CTTTGAGAACTGCTGGCTTAC
Cebus_551_016107345_9840148	tAGTTGCCCTGGAGTGAGAG	TTTAGGACAAAGGCCACGTAC
Cebus_621_016107351_6900083	CTACATTGCAGGGTGGGAATAG	GGAAGCACTACATGGCAAATC
Cebus_738_016107358_8091150	TGGGGTCTAGTGGCTTAGTTG	CCCAAACCCCATTCTTTCCTG
Cebus_763_016107360_14366294	ACAGAGGTCTTCGGAGGATTG	GgAGCCAAGTGTGAAAAGGAC
Cebus_806_016107363_2740619	AAAAGGCCAAGCAgTTAGGAC	CACAAATGTCCcTGAGCAGAG
Cebus_860_016107366_7356484	CGCCCATCTCTGTATCAAAGC	ACCAGCTTTCTTTGCAGCTAG
Cebus_917_016107371_2525009	ACAGCAGGCAAAATAGAAGAGG	AGGCTCAGATTCTCACAATGC
Cebus_1021_016107380_1842784	cTGATGTTTCTCAcGGTTATGC	CCATTTCCACAGCCACTAACC
Cebus_1105_016107386_2160268	GTTTTGGTGAATCTCCCCTCTG	AATCaCTCTGCTGGGGTTTTG
Cebus_1173_016107392_6561526	TTTTCAGGCTGCTTGGATCTG	AGAACgGGTCTCCAAAATCC
Cebus_1193_016107394_2513331	TGCAACATTtCTCAGGCTTGG	ACCTCCCTGATCTTGACATCC
Cebus_1366_016107408_1098227	CTCTTTGATGCCTTCgTCCTG	TGCAGCATTTCACtTCGACTG
Cebus_1371_016107409_1795398	CTCTGCAGGGAATCACACAC	AAAGCCATGAGACAACCTGTG
Cebus_1404_016107413_1061124	AcATTTCAGGaGTTGGCAGTG	TGAAGTCTCTGGATTCCTAGTCC
Cebus_1487_016107424_3074456	GCAAAGAAACAGCCACTACTAC	CAAAGTTGGGGAAATGAGGTC
Cebus_1494_016107424_649155	CCgGCTTTGCATATTTTCTGTG	CTCCaAGGCCTGTAGACATTC
Cebus_1551_016107432_597944	AGATCTCACTAGCCTGCCAAC	ATTTCAGACCATGCCTGCTTC
Cebus_1668_016107447_4848221	TATCAACTGTTGGCTGGAAGG	CAGAAGAAGCCCAGcGAATTG
Cebus_1681_016107450_2122366	CTGGTGTTAAGTCTGGGCTTC	TCCTTCCCTTAGACACCAGAG
Cebus_1697_016107452_354656	CTGGGCGCTTCTTACCAATAC	GGAGGTGTATTCATAGCCCTTC
Cebus_1736_016107457_370296	TTACAGGTGCAGGTCAAGAAC	GGACTACTCAgCTTCAAAGGG

Cebus_1774_016107463_2414412	GCAAGGAAGCAGTGACTTTG	ACTTGCAGCAGGAAAGGTTG
Cebus_1848_016107473_3066026	CTGGACAGATAAAGCCCATGAC	GTGCCCTTTGGTAGTCTGTTC
Cebus_1992_016107501_1530125	GGGCAGGTgAAGGAAATATCTC	GGGAGTGTCAGgGCAATTTG
Cebus_2074_016107513_2195588	AGCAGAcCCAGATGAAATGAG	CACTTAGCATCCCCACTTGAC
Cebus_2119_016107520_2421452	CCTTTGGGCAGAACTAGAAGC	AAGGCAGCAGAAGTTAAAGGG
Cebus_2131_016107521_820781	ATGGCCAGAAcgAGTCAAAAC	GAGAATGTGCCCTGTCATGTC
Cebus_2147_016107526_2013625	AGTTaTTACTTGGGCTGGTGTG	TGTTGCATGCTTATGACCTTCC
Cebus_2355_016107570_538805	AcATGGGCACTTGAGTTTCTG	AAGGGCTgCATGAGATGATTC
Cebus_2390_016107575_1308169	TTCAAGGGCAGAGACCACAAC	TGACTCTTCAGCTGGGATCC
Cebus_2461_016107586_2510294	CTATGGGAAACAGcGCTGAG	TTTTGGAGGCCTGTCATTTGG
Cebus_2509_016107599_118541	TCTGTTCCTCACACTCCATGG	CTGCCAAAGAAaAGCTCAACC
Cebus_2591_016107614_2535385	CACAGGAGGCAGGTATTTCATC	AGAAGGAAGAGGGAAAGAGAGG
Cebus_2599_016107619_1494508	TGTAGCATGCAGAgTGTCAAG	GTGgCCACTTCTAGCAATATCC
Cebus_2608_016107623_1314989	GTAATGACAACAGCTTCTAGGC	CTGTATCAGTGCCAGTTTCTCC
Cebus_2682_016107643_2443408	CTGAAAAGcTGCAAGGTACAAC	GGAGATTTTGGTTGGGATTGC
Cebus_2711_016107653_262260	AAAGTGCAGGATGTGTCTGTG	CAGCAGGCTCTTTCAGGTTC
Cebus_2732_016107658_957071	GTTAACAGAGGCAGTGTGGAG	GGCTGTACTGCTgTCTACAAC
Cebus_2765_016107666_419176	GGTTCAaTCTTCCACCCACAG	GGCACCAGTCAACCATTTAAC
Cebus_2854_016107696_621273	TTGACTGCAATGATCAGAGTCC	ATGCCACCCTCTCAACACAC
Cebus_2855_016107696_621273	TTGACTGCAATGATCAGAGTCC	ATGCCACCCTCTCAACACAC
Cebus_2865_016107700_1462157	TGAGAATGTCCTGTGGGTGTG	ACTGACCCCTAAGCAATCCTG
Cebus_2938_016107730_149900	TGCTGAACAATGCAAAGGAC	CAGGGCTGGGTTTTCATTTTC
Cebus_3066_016107777_780084	CCCAtGTGTCATTGGCTCTC	CCAGATCAGGGCTTAGATCAC
Cebus_3115_016107806_768864	AGTCCTGTTCCCTGAGTCTTC	GTCCCATATCCAAGGCTGAAG
Cebus_3125_016107814_187558	TCCACTCTTTGACTCCTTCCC	AGTGGGAGAAGGGTGTGTTAG
Cebus_3230_016107875_595146	GGGAGACATCAAGGTGGTTTC	ACCATtTAGAGAGGCCCTGAG
Cebus_3300_016107947_11006	TTGGCTCATTCGAAGTTCTCC	TGGCCAGTGTTAGCAATAAGG
Cebus_3318_016107956_562232	AGCCAGCTTTCTCTCAACATC	CcGAACTACCCTTGTGTCTC
Cebus_3428_016108143_152691	CCAGGCTGAAAAGACTCACAG	TTTTCCAgCCTCCAGTTTTGC
Cebus_3463_016107316_1117546	ACACACATCTCTGATCACCTTG	GGCTaTACATGCCACCTGTTTC
Cebus_3583_016107333_3694470	CTCCTGCCTCCTGATTTGTTG	CACTACACTTGTTCCGACTCC
Cebus_3651_016107345_10587979	CTGGAGAAAGCAGTGGTGATG	ACcCAGTGAATCCTCTCTTCC

Cebus_3766_016107365_1761950	AGCCTGAATGCATGTCTCTTG	GAGTTGCCAATAATCCCTTGTG
Cebus_3938_016107402_5335929	GCATAGCCAGATTCCCAAAGG	CCTCATCAGCTTCCCATATCC
Cebus_3951_016107409_1902489	AATGTTTGGTCCcAGCTACAC	AAGCTAACAGGAGTGGTACCC
Cebus_4058_016107444_744647	ACCCATGCATAGAAGGGGATC	CAAAGGCAGtCTGGTCACAC
Cebus_4119_016107472_463561	ACTTTGCCCATCAGCCAGTC	GTGTTGAGCTAAGCCAGTCTG
Cebus_4161_016107498_700474	AAGACCTCCCTAGCCAAGTTC	CTTTTCCAGCAaCCTCTTCCC
Cebus_4172_016107504_1207046	ATGGACAGTGCTTTTGGTGTC	CCAAATCACAGCAGGTTTTGG
Cebus_4210_016107518_2173971	GCAGGAGATGAAGGTGGTAAG	GAGTTGGCTGCAAATTTCTGTC
Cebus_4226_016107528_1641570	TTGGGCCTGTTGATCTTTAGC	AACTTCTGTCCTGGCTTTTCG
Cebus_4364_016107602_1144387	TCCACCCTTCTCCACATATCTC	AGCTGAGGGAGTCTAGCATAAG
Cebus_4525_016107740_934103	CAGCTCTCTCTTTTGCAGACC	GCATTTAGGGATGAGCTGTAGG
Cebus_4527_016107742_1227275	CTGCTGTTGTCTGAGGAATGG	AGAGAATGGGGAAGCAAGAGG
Cebus_4534_016107747_847239	GGCTCACTTTCCTGTCTTTTG	AAGCTGGCCCCTTGAaATTAC
Cebus_4772_016107481_1550445	AATGGCATTTCTGGAGCTCAC	CACgCAGAGGGGAATTACTC
Cebus_4869_016107323_10330746	GGAATGCAGGGTTGGTTTAATG	CCTTAcGGCACTGTTTAGAACC
Cebus_4904_016107330_1488926	CCCAGGGAAATTCAGACACAG	CAGACCCCACATCTTGTTAACC
Cebus_4980_016107354_9467046	TCTCTGTCATTTTGGCCACTC	CTGCCcTGAAATTCCATGGG
Cebus_5070_016107379_3496758	CTTCAGCCTCAACTTCCCATC	TTAGCCAGAACTCCCCTTACC
Cebus_5075_016107381_3781736	AGGATTGCTTGCATGGTTGTG	ACAGTCACcAAATCCCAAACC
Cebus_5085_016107382_6296694	CCTCTGTCCTGCATTCTTTCAG	TAACATGCAGCAACTCACCAG
Cebus_5091_016107383_6617877	cACCCATTCAATCACCTAGGG	GGTGAGAAAATGGAGCAGAATC
Cebus_5205_016107418_2904436	CTGGCACTGAGAAAGGATGTG	TCCACTGCATGTTCTgTAAGC
Cebus_5259_016107445_279668	ACTGTGTGTTGTGTGGGAAAG	AGCATGGATTCTGGGACTAAC
Cebus_5323_016107473_4499228	GCAAAATTTCAGGTCCCATCG	TTGTAAGTGATGGCAGCTGAG
Cebus_5584_016107688_1399079	ATCCTACATTGCTGCCATCTG	ACCTGcCAAAAGTCACTTAGC
Cebus_5603_016107715_1574316	TtGGGGCCTAATTTTGGATGG	AGGGGATCAGAAGTCAACCAG
Cebus_5639_016107780_396464	CAGGGCTTAATTGGTCCATGG	GCGTTCTGGAAGGTACATGTC
Cebus_5651_016107794_1274094	GCTGCCTAAACCTCAGGATTG	GTAACTAGCTCgGCATCACAG
Cebus_5662_016107809_762248	AGGACTTAAATGGAGGGCTTTC	TAGCTTTGAGTGGGGAGGAG

Cebus_5730_016107974_704527	ATGTGTGAGATGCgGCTAAAG	AGTAGTTTGCCCTGTGACCTC
Cebus_5756_016108092_68189	GTGTGGGGTTGTGTGTTACC	TCTGTCACCTCTAGCcATGTC
Cebus_5782_016107421_3233984	CCCTTTGTTTCTTGGGTTTGC	AGCCTCACATCCTTTTGTCTTC
Cebus_5800_016107692_2062462	AGAGTTTGCCCTTTGAACCTC	TATGCACCAAAAGGACCTGTG
Cebus_5824_016107372_4314224	ATCCTGGTTCCTAcGGATCTC	TCCAAATAGCCCAGGATCTCC
Cebus_5846_016107507_1130389	AGACAGCGAGACAAGGACAAG	TCTTTGAGACAGAACAGCCAAC
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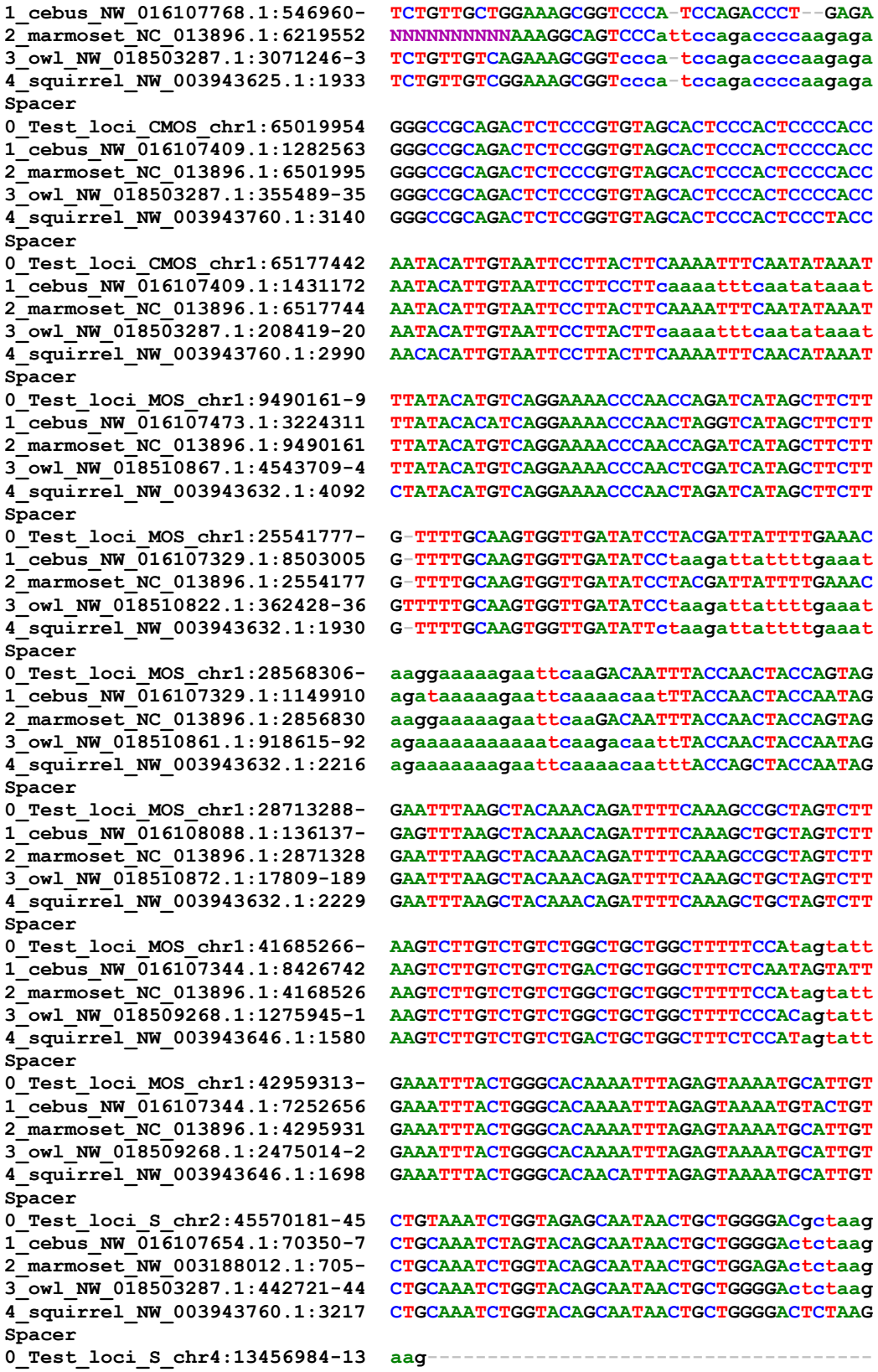
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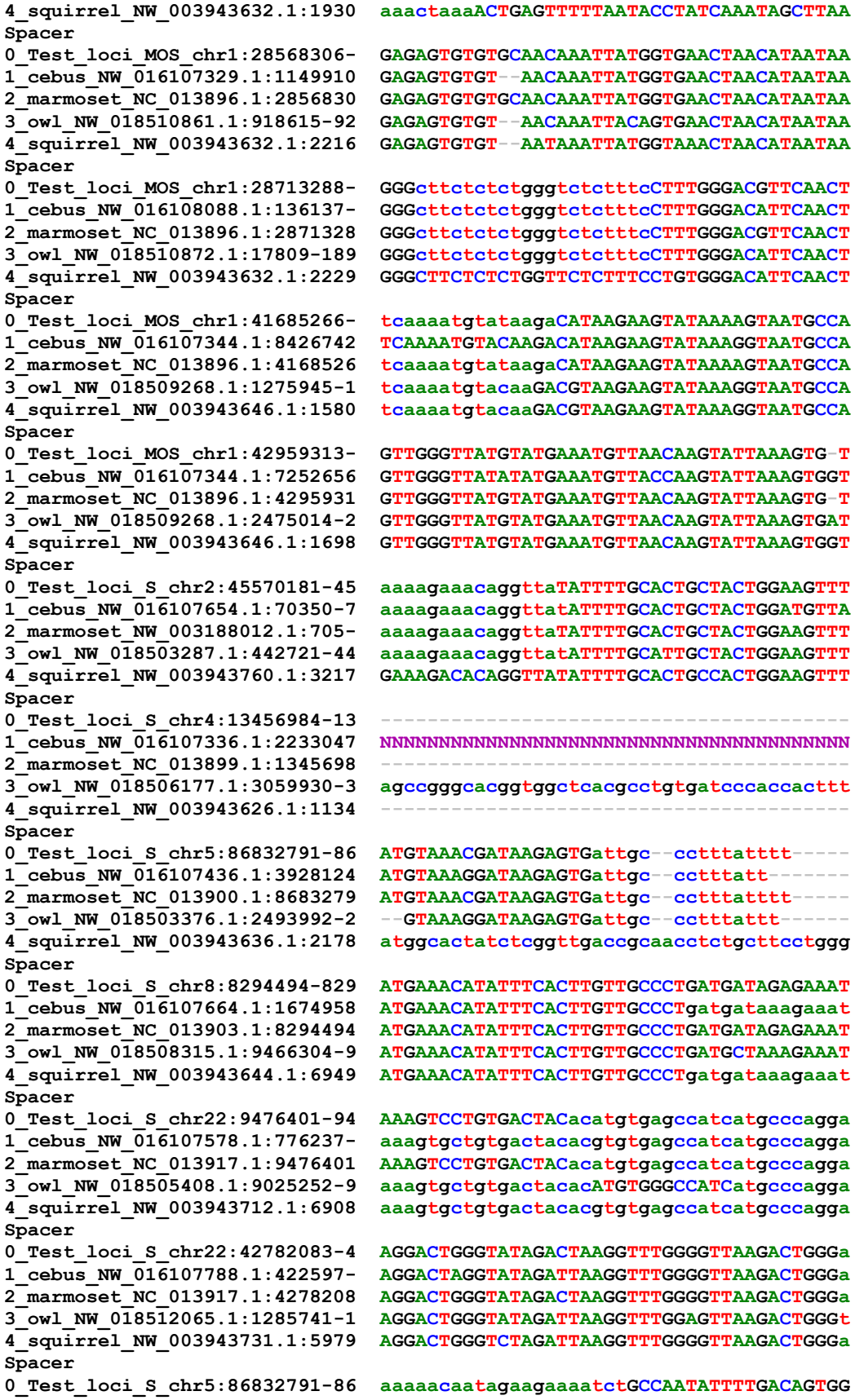
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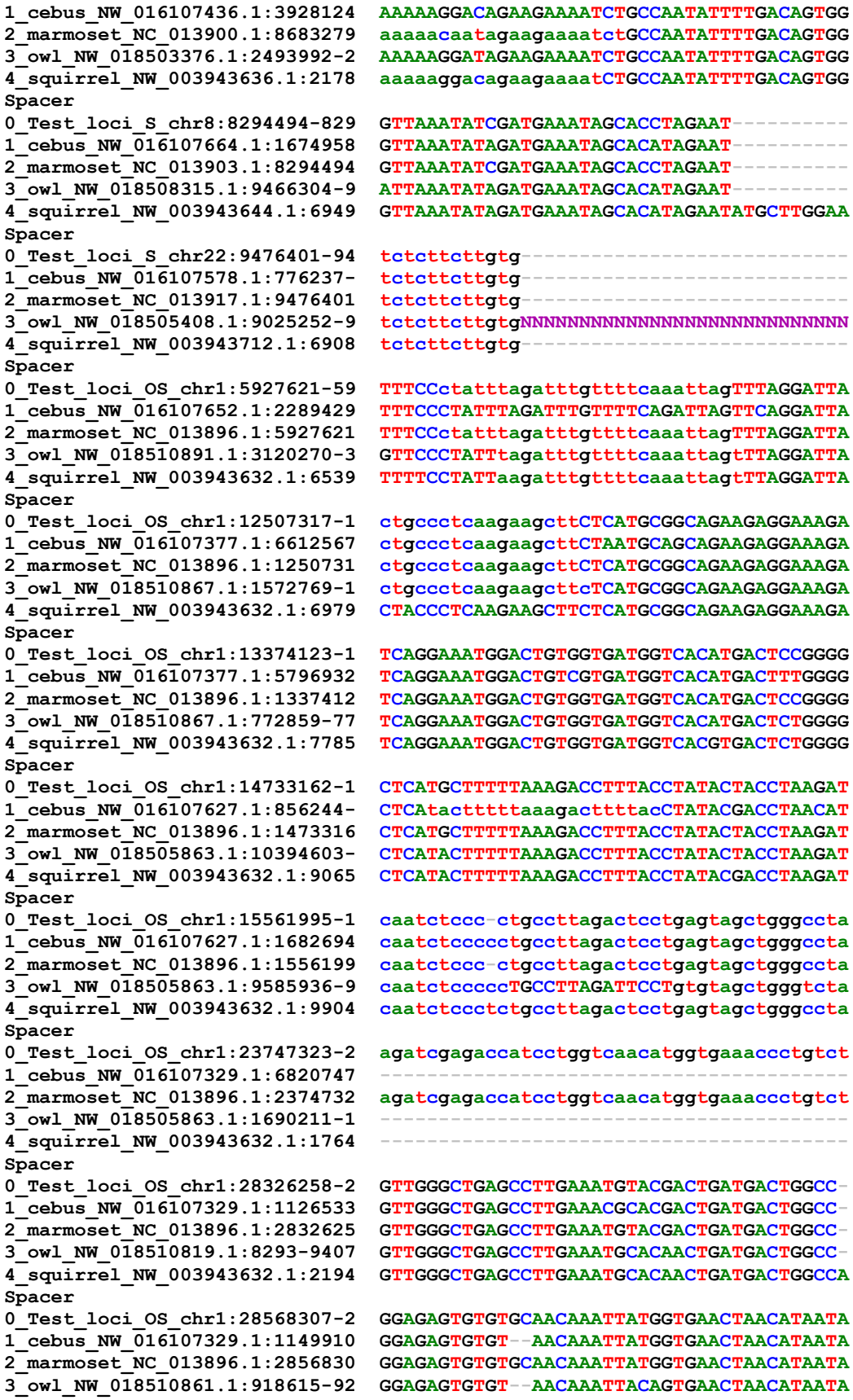
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2_marmoset_NC_013903.1:8294494  ------------------TATACTGTTTCCAAGC------
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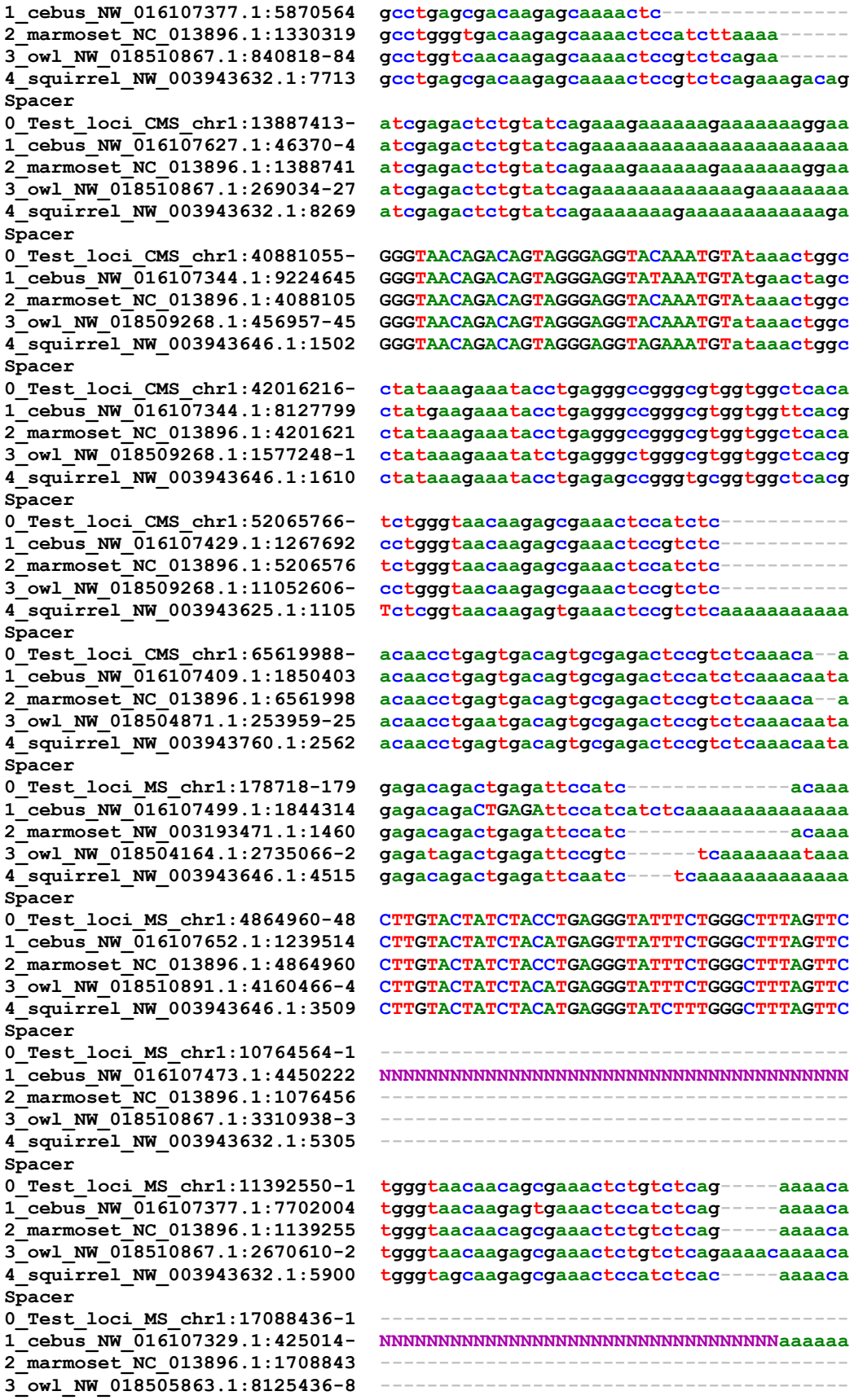
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3_owl_NW_018510867.1:696877-69  ---------agcaagactccatctc---------------
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4_squirrel_NW_003943636.1:2178  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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4_squirrel_NW_003943636.1:2178  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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3_owl_NW_018510891.1:3120270-3  ctccagcctgggtaactctgtctcaaaa------------
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3_owl_NW_018510867.1:772859-77  gagccaagattgtgccattgcactccagcctgggcaacag
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3_owl_NW_018505863.1:1690211-1  GGGTCTGCATTTCCTGAATCAACAGATACTTCAACTGGTT
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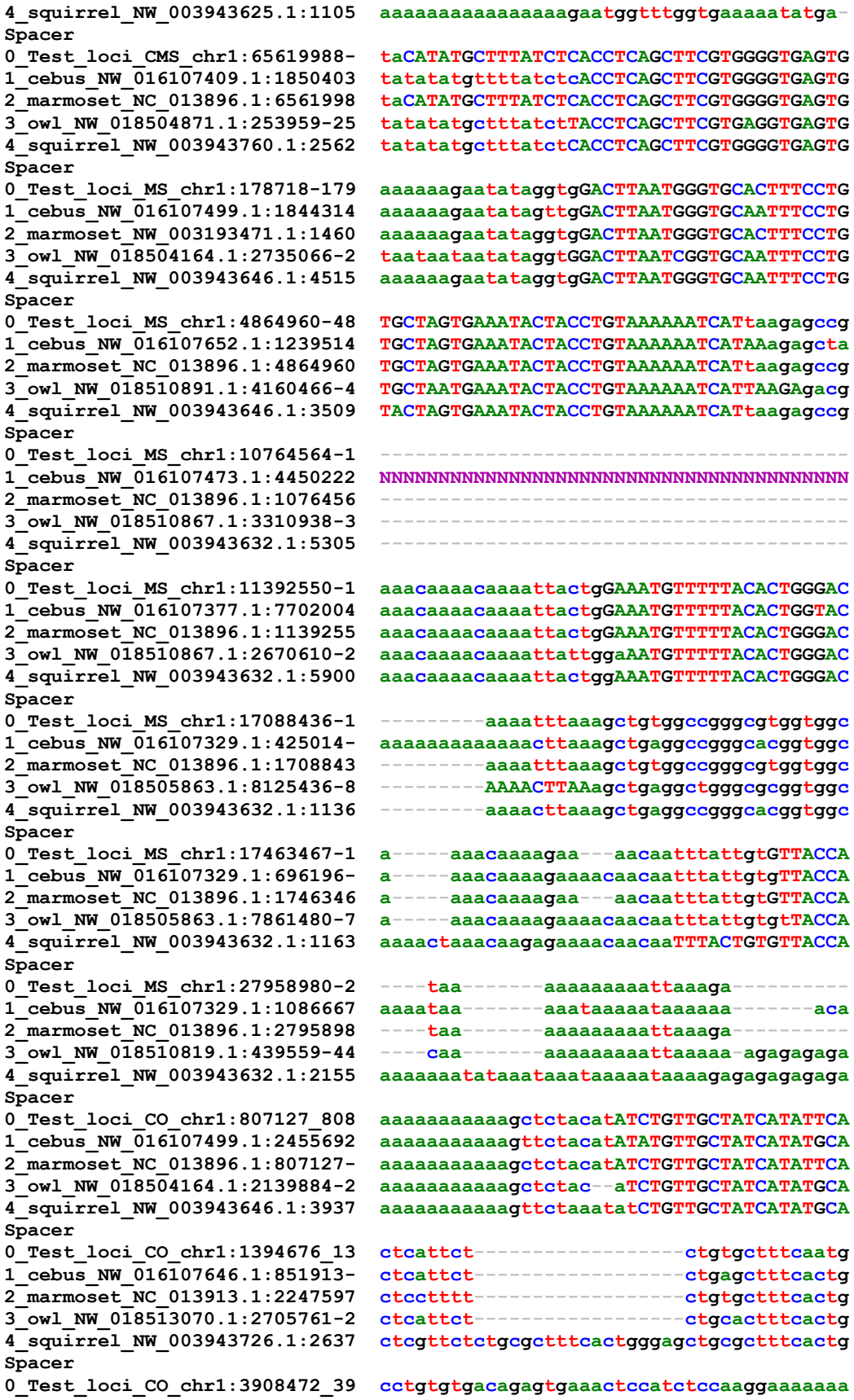
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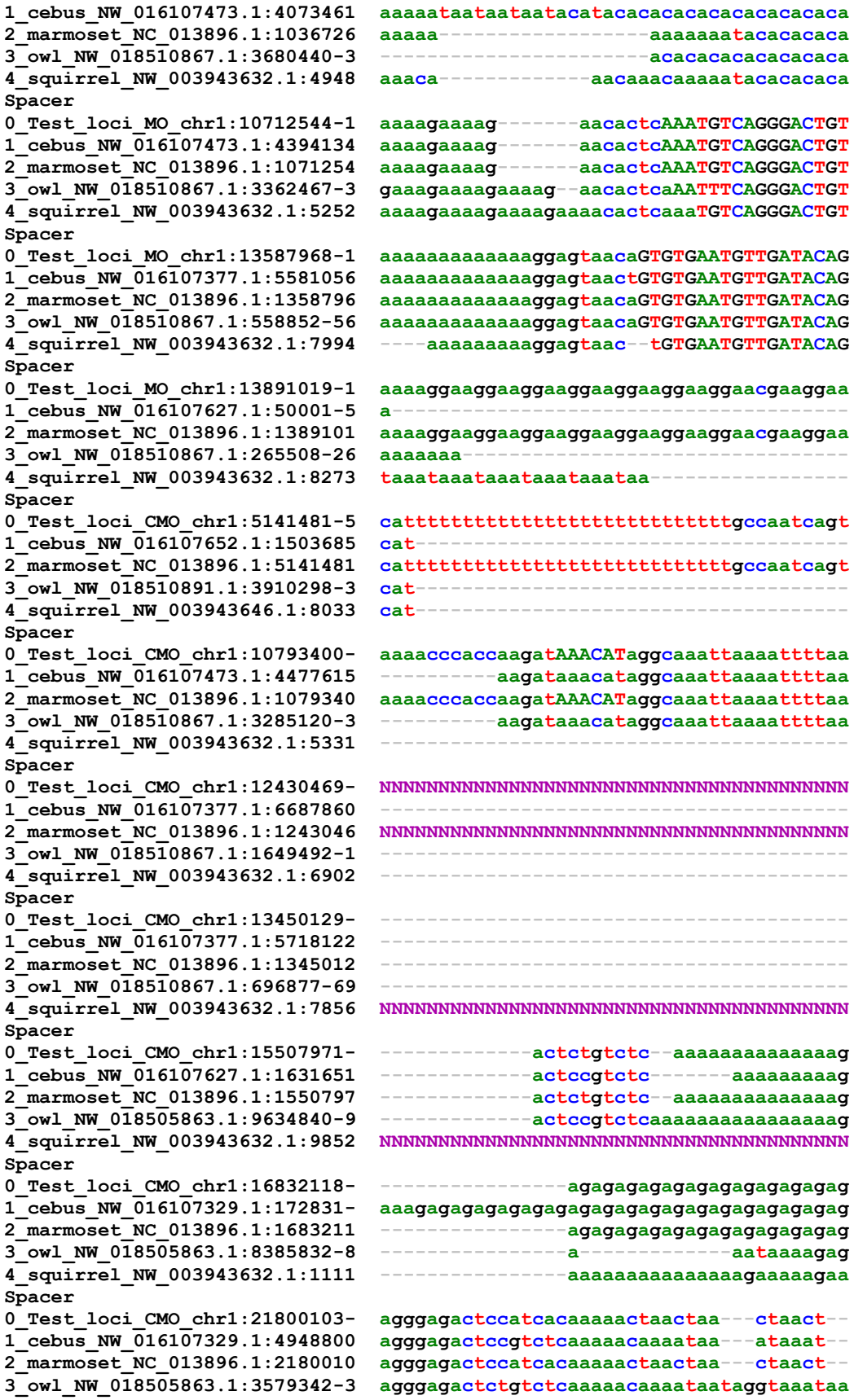
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4_squirrel_NW_003943632.1:5252 aaaagaaaagaaaagaaaacactcaaaTGTCAGGGACTGT
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0_Test_loci_MO_chr1:13587968-1 aaaaaaaaaaaaaggagtaacaGTGTGAATGTTGATACAG
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2_marmoset_NC_013896.1:1358796 aaaaaaaaaaaaaggagtaacaGTGTGAATGTTGATACAG
3_owl_NW_018510867.1:558852-56 aaaaaaaaaaaaaggagtaacaGTGTGAATGTTGATACAG
4_squirrel_NW_003943632.1:7994 ----aaaaaaaaggagtaac--tGTGAATGTTGATACAG
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0_Test_loci_MO_chr1:13891019-1 aaaaggaaggaaggaaggaaggaaggaaggaacgaaggaa
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2_marmoset_NC_013896.1:1389101 aaaaggaaggaaggaaggaaggaaggaaggaacgaaggaa
3_owl_NW_018510867.1:265508-26 aaaaaaa----------
4_squirrel_NW_003943632.1:8273 taaataaataaataaataataa----------
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0_Test_loci_CMO_chr1:5141481-5 catttttttttttttttttttttttttttgccaatcagt
1_cebus_NW_016107652.1:1503685 cat----------
2_marmoset_NC_013896.1:5141481 catttttttttttttttttttttttttttgccaatcagt
3_owl_NW_018510891.1:3910298-3 cat----------
4_squirrel_NW_003943646.1:8033 cat----------
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0_Test_loci_CMO_chr1:10793400- aaaacccaccaagatAAACATaggcaaattaaaattttaa
1_cebus_NW_016107473.1:4477615 ----------aagataaacataggcaaattaaaattttaa
2_marmoset_NC_013896.1:1079340 aaaacccaccaagatAAACATaggcaaattaaaattttaa
3_owl_NW_018510867.1:3285120-3 ----------aagataaacataggcaaattaaaattttaa
4_squirrel_NW_003943632.1:5331 ----------
Spacer
0_Test_loci_CMO_chr1:12430469- NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
1_cebus_NW_016107377.1:6687860 ----------
2_marmoset_NC_013896.1:1243046 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
3_owl_NW_018510867.1:1649492-1 ----------
4_squirrel_NW_003943632.1:6902 ----------
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0_Test_loci_CMO_chr1:13450129- ----------
1_cebus_NW_016107377.1:5718122 ----------
2_marmoset_NC_013896.1:1345012 ----------
3_owl_NW_018510867.1:696877-69 ----------
4_squirrel_NW_003943632.1:7856 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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0_Test_loci_CMO_chr1:15507971- ----------actctgtctc--aaaaaaaaaaaaaag
1_cebus_NW_016107627.1:1631651 ----------actccgtctc-------aaaaaaaaag
2_marmoset_NC_013896.1:1550797 ----------actctgtctc--aaaaaaaaaaaaaag
3_owl_NW_018505863.1:9634840-9 ----------actccgtctcaaaaaaaaaaaaaaag
4_squirrel_NW_003943632.1:9852 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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0_Test_loci_CMO_chr1:16832118- ----------agagagagagagagagagagag
1_cebus_NW_016107329.1:172831- aaagagagagagagagagagagagagagagagagagag
2_marmoset_NC_013896.1:1683211 ----------agagagagagagagagagagag
3_owl_NW_018505863.1:8385832-8 ----------a----------aataaaagag
4_squirrel_NW_003943632.1:1111 ----------aaaaaaaaaaaaaaagaaaaagaa
Spacer
0_Test_loci_CMO_chr1:21800103- agggagactccatcacaaaaactaactaa---ctaact--
1_cebus_NW_016107329.1:4948800 agggagactccgtctcaaaaacaaaataa---ataaat--
2_marmoset_NC_013896.1:2180010 agggagactccatcacaaaaactaactaa---ctaact--
3_owl_NW_018505863.1:3579342-3 agggagactctgtctcaaaaacaaaataataggtaaataa

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4_squirrel_NW_003943632.1:1581  NNNNNNNNNNNNNNNNNNaaataaataaataaataaaaat
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0_Test_loci_CMO_chr1:30626199-  aaatcaagaccatcctggtcaacatggtgaaaccccatct
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2_marmoset_NC_013896.1:3062619  aaatcaagaccatcctggtcaacatggtgaaaccccatct
3_owl_NW_018504164.1:3855738-3  agatcaagaccatcctggtcaacatggtgaaaccctgtct
4_squirrel_NW_003943646.1:5568  agattgagaccatcctggtcaacatggtgaaaccctgtct
Spacer
0_Test_loci_CMO_chr1:35055006-  GTGAGTTTAAACCATTTAAAAgttttgtggccgggcgcgg
1_cebus_NW_016107980.1:307170-  GTGAGTTTAAaccatttaaaagttttatggccagatacag
2_marmoset_NC_013896.1:3505500  GTGAGTTTAAACCATTTAAAAgttttgtggccgggcgcgg
3_owl_NW_018504164.1:8121233-8  GTGAGTTTAAaccatttaaaagttttatggccgggcacag
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0_Test_loci_CMOS_chr1:12318704  ------------------------------aaacccaac
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2_marmoset_NC_013896.1:1231870  ------------------------------aaacccaac
3_owl_NW_018510867.1:1757948-1  -------aaacaaaaaacaaaaaacaaaaaaaaccccaac
4_squirrel_NW_003943632.1:6792  ---CCCccaaccaaaaacaacaacaacaacaacaaaaaac
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0_Test_loci_CMOS_chr1:13194634  aaaaagaaaaaa-aaaacaacaaaggaaaaacaacaacaa
1_cebus_NW_016107377.1:5966208  agaaagaaaaaagaagaaaaagaaacaacaacaacaacaa
2_marmoset_NC_013896.1:1319463  aaaaagaaaaaa-aaaacaacaaaggaaaaacaacaacaa
3_owl_NW_018510867.1:938736-93  agaaaaagaaaa---------------acaacaacaataa
4_squirrel_NW_003943632.1:7612  aaaaaaaaaaaagaagaagaaaaagagaaaacaacaacga
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0_Test_loci_CMOS_chr1:27268200  tgagaccatcctggccaacatggtgaaaccccgtctccac
1_cebus_NW_016107329.1:1020309  cgtgaccatcctggccaacatggtgaaaccccgtttctac
2_marmoset_NC_013896.1:2726820  tgagaccatcctggccaacatggtgaaaccccgtctccac
3_owl_NW_018510819.1:1096308-1  cgagaccatcctggccaacatggtgaaattccatctctat
4_squirrel_NW_003943632.1:2093  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_CMOS_chr1:54627261  aaacaacaacaacaaaaaaaaactgtactgCTAAAGAAAT
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2_marmoset_NC_013896.1:5462726  aaacaacaacaacaaaaaaaaactgtactgCTAAAGAAAT
3_owl_NW_018509268.1:13535416-  ----------taaaaaaaaaaactgtactgCCAAAGAAAT
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Spacer
0_Test_loci_CMOS_chr1:58607516  -----gaacaaaaaaaaaaaaagaatttggattaTAAGTA
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2_marmoset_NC_013896.1:5860751  -----gaacaaaaaaaaaaaaagaatttggattaTAAGTA
3_owl_NW_018487996.1:3450606-3  aaaaaaaaaaaaaaaaaaaaaaagaatttggattCTAAGTA
4_squirrel_NW_003943625.1:5169  --aaaaaaaaaaaaaaaaaaagaatatgaattgTAAGTA
Spacer
0_Test_loci_CMOS_chr1:62195522  gtctcaaaagaaaagaaagtaaagaaataaagaatggtaG
1_cebus_NW_016107768.1:546960-  gtctcaaaag-aaagaaagtaaagaaataaagaatggtaG
2_marmoset_NC_013896.1:6219552  gtctcaaaagaaaagaaagtaaagaaataaagaatggtaG
3_owl_NW_018503287.1:3071246-3  gtctcaaaagaaaagaaagtaaagaaataaagaatggtaC
4_squirrel_NW_003943625.1:1933  gtctcaaaag-aaagaaagtaaagaaataaagaatggtaG
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0_Test_loci_CMOS_chr1:65019954  ------------------------------aaacaaaa
1_cebus_NW_016107409.1:1282563  ------------------------------at------
2_marmoset_NC_013896.1:6501995  ------------------------------aaacaaaa
3_owl_NW_018503287.1:355489-35  aaaaaaaaaactaaaaaacaaaacaaaacaacaaaaaaaa
4_squirrel_NW_003943760.1:3140  ------------------------------aaaaaaaa
Spacer
0_Test_loci_CMOS_chr1:65177442  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
1_cebus_NW_016107409.1:1431172  -----------------------------------------
2_marmoset_NC_013896.1:6517744  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
3_owl_NW_018503287.1:208419-20  -----------------------------------------
4_squirrel_NW_003943760.1:2990  -----------------------------------------
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0_Test_loci_MOS_chr1:9490161-9  aattacccaaCTCTCTATGGTTGCCATGTTGCaattctta
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1_cebus_NW_016107473.1:3224311  aattacctgactCTCTATGGTTGCCATGTTGCAATTCCTA
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3_owl_NW_018510867.1:4543709-4  aattat----ctctctaTGGTCGCCATGTTGCAATTCCTA
4_squirrel_NW_003943632.1:4092  aattacctgactCTCTATGGTTGCCATGTTGCAATTCCTA
Spacer
0_Test_loci_MOS_chr1:25541777-  gagtgagattctgtctcaaaaaaaaa--------------
1_cebus_NW_016107329.1:8503005  gagtgagattctgtatcaaa-----------------
2_marmoset_NC_013896.1:2554177  gagtgagattctgtctcaaaaaaaaa--------------
3_owl_NW_018510822.1:362428-36  gagtgagattctgtctcaaaaaa----------------
4_squirrel_NW_003943632.1:1930  cagtgagactctgtttcaaaaaaaaaaaaaagaaaaatac
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0_Test_loci_MOS_chr1:28568306-  gcaagcctccgtctc----------aaaaaaaagagaaa
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2_marmoset_NC_013896.1:2856830  gcaagcctccgtctc----------aaaaaaaagagaaa
3_owl_NW_018510861.1:918615-92  gtgagactccgtctc-----------aaaaaaaaagaaa
4_squirrel_NW_003943632.1:2216  gcgagactccatctcaaaaaaaaaaaaaaaaaaaagaaa
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2_marmoset_NC_013896.1:2871328  aacaaaaatgaaattccatctc-aaaaaaaagaaaaagaa
3_owl_NW_018510872.1:17809-189  aacaaaaatgaaactccatctc--aaaaatagaaaaagaa
4_squirrel_NW_003943632.1:2229  aacaaaaatgaaactccatctcaaaaaaaaagaaaaagaa
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3_owl_NW_018509268.1:1275945-1  tcacccaggctggagtgcagtggtgtgatcctggctcact
4_squirrel_NW_003943646.1:1580  tcacccaggctggagtgcagtggcgtgatcttggctcact
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0_Test_loci_MOS_chr1:42959313-  ggtgacacagcaagactctgtctccaa-------------
1_cebus_NW_016107344.1:7252656  agagtcagagcaagactctgtctcagaaaaaaaa------
2_marmoset_NC_013896.1:4295931  ggtgacacagcaagactctgtctccaa-------------
3_owl_NW_018509268.1:2475014-2  ggtgacagaggaagactccgtatcaaaaaaaaaaaaa---
4_squirrel_NW_003943646.1:1698  ggcggcagagcaagactctctcaaaaaaaaaaaaaaaga
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0_Test_loci_S_chr2:45570181-45  GTATTACATTAGTATTAGAAGCAACGGTGTGGATATTAGG
1_cebus_NW_016107654.1:70350-7  GTATTACATTAGTATTAGAAGCAACAGTGTGGATATCAGA
2_marmoset_NW_003188012.1:705-  GTATTACATTAGTATTAGAAGCAACTATGTGGATATTAGA
3_owl_NW_018503287.1:442721-44  GTATTACATTAGTATTAGAAGCAACAGTGTGGATATTAGA
4_squirrel_NW_003943760.1:3217  GTATTACATTAGCATTAGAAGCGACAGTGTGGATATTAGA
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0_Test_loci_S_chr4:13456984-13  AAAATGTAACCAGCTAGGAGGCCTAGTGAGGAGGCTGAAC
1_cebus_NW_016107336.1:2233047  AAAATGTAACCAGCTAAGAGGCCTAGTGAGGAGGCTGAAC
2_marmoset_NC_013899.1:1345698  AAAATGTAACCAGCTAGGAGGCCTAGTGAGGAGGCTGAAC
3_owl_NW_018506177.1:3059930-3  ACAATGTAACGAGCTAGGAGGTCTAGTGAGGAGGCTGAAC
4_squirrel_NW_003943626.1:1134  AAAATGTAACCAGCTAGGAGGCCTCGTGAGGAGGCTGAAC
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0_Test_loci_S_chr5:86832791-86  ----------------------------------------
1_cebus_NW_016107436.1:3928124  ----------------------------------------
2_marmoset_NC_013900.1:8683279  ----------------------------------------
3_owl_NW_018503376.1:2493992-2  ----------------------------------------
4_squirrel_NW_003943636.1:2178  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_S_chr8:8294494-829  ----------------------------------------
1_cebus_NW_016107664.1:1674958  gccagcatgcccagctaatttttttttgtatttttattag
2_marmoset_NC_013903.1:8294494  ----------------------------------------
3_owl_NW_018508315.1:9466304-9  ----------------------------------------
4_squirrel_NW_003943644.1:6949  gccaccatgcccagctaa-tttttttgtatttttactag
Spacer
0_Test_loci_S_chr22:9476401-94  ----------------------------------------
1_cebus_NW_016107578.1:776237-  ----------------------------------------
2_marmoset_NC_013917.1:9476401  ----------------------------------------
3_owl_NW_018505408.1:9025252-9  ----------------------------------------
```

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4_squirrel_NW_003943712.1:6908  NNNN
```

```
1_cebus_NW_016107329.1:1126533  ------aaaaacaaaaaaggaaagaaaggtgaTTGGACGT
2_marmoset_NC_013896.1:2832625  ---aaaaaaaaaaagaaagaaagaaaggtgatgGGACAT
3_owl_NW_018510819.1:8293-9407  caaaaaaaaaaaaagaaaagaaagaaaggtgattGGACAT
4_squirrel_NW_003943632.1:2194  -----aaaaaaaaagaaaagaaagaaaggtgattGGACAT
Spacer
0_Test_loci_OS_chr1:28568307-2  agcaagcctccgtctc----------aaaaaaaagagaa
1_cebus_NW_016107329.1:1149910  agcaagactccgtctc---------caaaaaaaaaaagaa
2_marmoset_NC_013896.1:2856830  agcaagcctccgtctc----------aaaaaaaagagaa
3_owl_NW_018510861.1:918615-92  agtgagactccgtctc----------aaaaaaaaagaa
4_squirrel_NW_003943632.1:2216  agcgagactccatctcaaaaaaaaaaaaaaaaaaaagaa
Spacer
0_Test_loci_OS_chr1:29483707-2  tggccaggcatggtggttcacgcctgtaatcccagcactt
1_cebus_NW_016108018.1:448879-  tggccaggcacggtggttcacgcctgtaatcccagcactt
2_marmoset_NC_013896.1:2948370  tggccaggcatggtggttcacgcctgtaatcccagcactt
3_owl_NW_018510816.1:124750-12  tggccgggcacggtgtttcacgcctgtaatcccagcactt
4_squirrel_NW_003943632.1:2300  tggccgggcacggtggttcatgcttgtaatcccagcactt
Spacer

                                         450       460       470       480
                                ....|....|....|....|....|....|....|....|
0_Test_loci_CS_chr1:195028-196  tttt------------------------------------
1_cebus_NW_016107499.1:1857925  ttttt-----------------------------------
2_marmoset_NC_013896.1:195028-  tttt------------------------------------
3_owl_NW_018504164.1:2721648-2  tttt------------------------------------
4_squirrel_NW_003943646.1:4502  tttttacaaaaaaaattttttttttttttgagacggagt
Spacer
0_Test_loci_CS_chr1:5862923-58  ------------------------------------------
1_cebus_NW_016107652.1:2218496  tttctatgtccttgaggaatcgccacgctgtcttccacaa
2_marmoset_NC_013896.1:5862923  ------------------------------------------
3_owl_NW_018510891.1:3190510-3  ------------------------------------------
4_squirrel_NW_003943632.1:5890  ------------------------------------------
Spacer
0_Test_loci_CS_chr1:6494342-64  aaaggtgGCCCCTGATGGCTCAGCTTAGAGTCCACCCATT
1_cebus_NW_016107473.1:257712-  aaaggtgGCCCCTGATGGCTCAGCTTAGAGTCCACCCACT
2_marmoset_NC_013896.1:6494342  aaaggtgGCCCCTGATGGCTCAGCTTAGAGTCCACCCATT
3_owl_NW_018510891.1:2618705-2  aaaggTGGCCCCTGATGGCTCAGCTTAGAGTCCACCCACT
4_squirrel_NW_003943632.1:1162  aaaagtggccCCTGATGGCTCAGCTTAGAGTCCACCCACT
Spacer
0_Test_loci_CS_chr1:9260979-92  ggagaaataggaacacttttactctgctggtgggagtgta
1_cebus_NW_016111560.1:3248-40  ggggaaataggaacacttttacactgttggtgggagtgta
2_marmoset_NW_003197695.1:4556  ggagaaataggggacacttttacactgctggtgggaatgta
3_owl_NW_018514732.1:7642590-7  ggagaaataggaacacttttacactgttggtgggagtgta
4_squirrel_NW_003944826.1:815-  ggagaaataggagcacttttaca--gttggtgggagtgta
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0_Test_loci_CS_chr1:15472853-1  AAGGAATTAATACCAGGTTGAGTTAGTCATTTGTGAGCCA
1_cebus_NW_016107627.1:1597835  AAGGAATTAACACCAGGTTGAGTTAGTCATTTGTGAGCCA
2_marmoset_NC_013896.1:1547285  AAGGAATTAATACCAGGTTGAGTTAGTCATTTGTGAGCCA
3_owl_NW_018505863.1:9677452-9  AAGGAATTAACACCAGGTTGAGTTAGTCATTTGTGAGCCA
4_squirrel_NW_003943632.1:9818  AAGGAATTAACACCAAGTTGAGTTAGTCATTTGTGAGCCA
Spacer
0_Test_loci_CS_chr1:25916534-2  caaatacTACATACTAAAAATAACTCATTACCTATCTTAA
1_cebus_NW_016107329.1:8861914  caaatacTACACACTAAAAATAACTCATTACCTATCTTAA
2_marmoset_NC_013896.1:2591653  caaatacTACATACTAAAAATAACTCATTACCTATCTTAA
3_owl_NW_018510819.1:2499878-2  taaatacTACACACTAAAAATAACTCATTACCTATCTTAA
4_squirrel_NW_003943632.1:1965  caaacaCTACACACTAAAAATAACTGATTACCTATCTTAA
Spacer
0_Test_loci_C_chr1:79592358-79  ------------------------------------------
1_cebus_NW_016107368.1:9246226  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
2_marmoset_NC_013896.1:7959235  ------------------------------------------
3_owl_NW_018498471.1:2845643-2  ------------------------------------------
4_squirrel_NW_003943702.1:3598  ------------------------------------------
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0_Test_loci_C_chr5:111337575-1  ------------------------------------------
```

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1_cebus_NW_016107543.1:2445109  NNNN
```

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4_squirrel_NW_003943632.1:4195  aattcttaAAGTCTTTTTATGGTGgtagaaaatttttttct
Spacer
0_Test_loci_CMS_chr1:10789407-  ATACtgatgccgggcgcagtggctcacgcctgtaatctca
1_cebus_NW_016107473.1:4475133  ATACTgatgccgggtgcagtggctcacgcctgtaatccca
2_marmoset_NC_013896.1:1078940  ATACtgatgccgggcgcagtggctcacgcctgtaatctca
3_owl_NW_018510867.1:3287386-3  ATACTGATgcagggcgtgatggctcatgcctgtaatccca
4_squirrel_NW_003943632.1:5328  ATACtgatgccgggtgcggtggctcatgcctgtaatccca
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0_Test_loci_CMS_chr1:13303195-  aaaaagtcatgcTTAGTTTAAAGTATAAACCACTAACATA
1_cebus_NW_016107377.1:5870564  ----------------------------------------
2_marmoset_NC_013896.1:1330319  aaaaagtcatgcTTAGTTTAAAGTATAAACCACTAACATA
3_owl_NW_018510867.1:840818-84  aaaaagtgatgcTTAGTTTAATGTATAAACCACTAATGTA
4_squirrel_NW_003943632.1:7713  aaaaagtcatgcTTAGTTTAATGTATAAACCACTAATCTA
Spacer
0_Test_loci_CMS_chr1:13887413-  ------------------------------tctacCCCTG
1_cebus_NW_016107627.1:46370-4  agaaaaaaagaaaaaagaaaaaaaaagaactctaccCCTG
2_marmoset_NC_013896.1:1388741  ------------------------------tctacCCCTG
3_owl_NW_018510867.1:269034-27  ------------------------------tctacccTTG
4_squirrel_NW_003943632.1:8269  ----------------------aaagaactctacCCCTG
Spacer
0_Test_loci_CMS_chr1:40881055-  aggccgtggtgggcagatcacaaggtcaggagattgagac
1_cebus_NW_016107344.1:9224645  aggccatgctgggcagatcacaaggtcaggagattaagat
2_marmoset_NC_013896.1:4088105  aggccgtggtgggcagatcacaaggtcaggagattgagac
3_owl_NW_018509268.1:456957-45  aggctgtggtgggcagatcacaaggtcaggagattgagac
4_squirrel_NW_003943646.1:1502  aggccgtggcgggcagatcacaaggtcaggagattgagcc
Spacer
0_Test_loci_CMS_chr1:42016216-  catgaggtcaagagatcgagaccatcctgatcaacacagt
1_cebus_NW_016107344.1:8127799  catgaggtcaagagatggagaccatcctggtcaacatggt
2_marmoset_NC_013896.1:4201621  catgaggtcaagagatcgagaccatcctgatcaacacagt
3_owl_NW_018509268.1:1577248-1  catgaggtcaagagatcgagaccatcctggtcaacatggt
4_squirrel_NW_003943646.1:1610  catgaggtcaagagattgagaccatcccggtcaatatggt
Spacer
0_Test_loci_CMS_chr1:52065766-  ----------------------------------------
1_cebus_NW_016107429.1:1267692  taaaatatcatGCTTTACACCCTTTACATTCAAGTCAAGA
2_marmoset_NC_013896.1:5206576  ----------------------------------------
3_owl_NW_018509268.1:11052606-  taaaatatcatGCTTTACACCCTTTATATTCAAGTCAAGA
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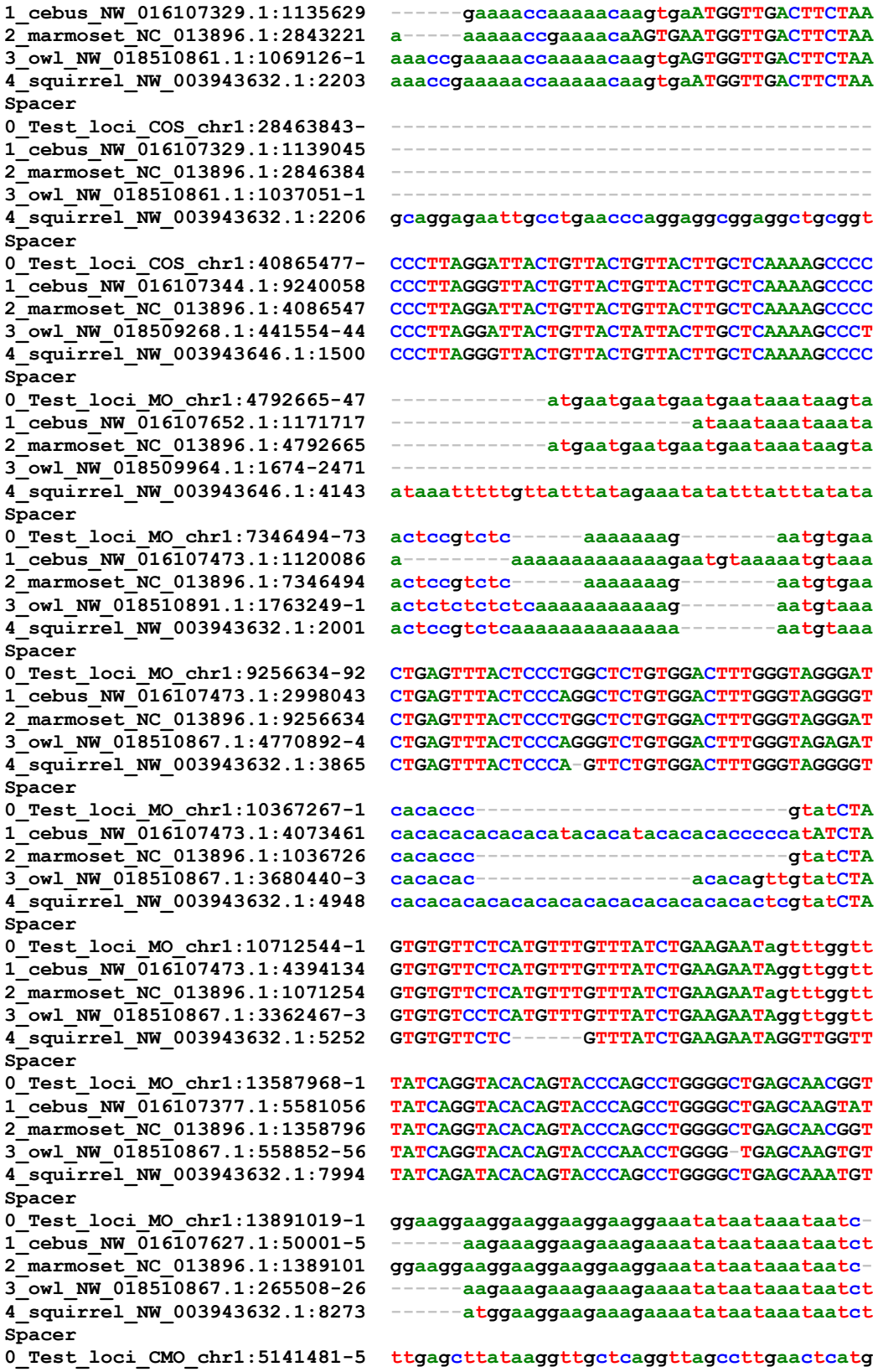
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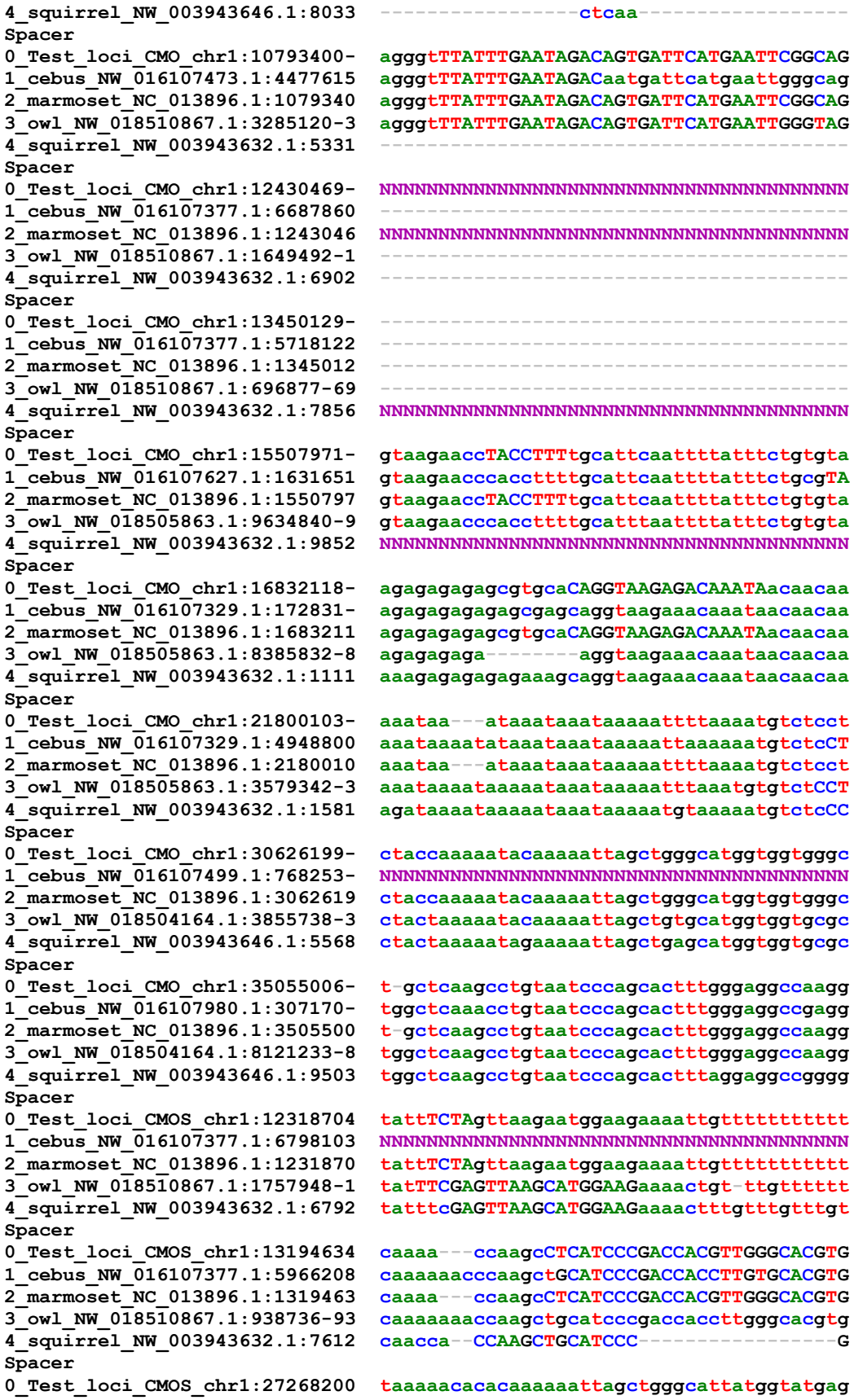
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0_Test_loci_CMOS_chr1:12318704 tatttCTAgttaagaatggaagaaaattgtttttttttt
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3_owl_NW_018510867.1:1757948-1 tatTTCGAGTTAAGCATGGAAGaaaactgt-ttgttttt
4_squirrel_NW_003943632.1:6792 tatttcGAGTTAAGCATGGAAGaaaactttgtttgtttgt
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4_squirrel_NW_003943636.1:2178  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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4_squirrel_NW_003943644.1:6949  agacagagtttcaccattttgatcaggatggtctctatct
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4_squirrel_NW_003943632.1:6539  aaaaccatGTATTTACATAGTTATAAATCTGATTATCTCC
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0_Test_loci_OS_chr1:12507317-1  attagctgggcacggtggcgcgtgcctgtaatcccagcta
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3_owl_NW_018510867.1:772859-77  gtGAATTGCATGGTTTATAAATGATATGGAATAAAGCAGT
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2_marmoset_NC_013896.1:2374732  AGCCTTTATCCCTTTGCAACCTTGAAACTACCTTGGTTGA
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2_marmoset_NC_013896.1:2832625  CAGCCCACAGGGATGCACTTACACCTGCATTATTCATAAA
3_owl_NW_018510819.1:8293-9407  CAGCTCACTGGGATGCACTTACACCTGCATTATTCGTAAA
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4_squirrel_NW_003943632.1:1962  ----------------------
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0_Test_loci_CM_chr1:13861977-1  ATTCACTGAAGCTAGGAGAGA
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3_owl_NW_018486157.1:485-1603   ATAAAAGCAACTCTGTTTCTA
4_squirrel_NW_003943632.1:9961  ATAAAAGCAACTCTGTTTCTA
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3_owl_NW_018505863.1:7282605-7  TTGACCTAGAAGTGCAGTGGA
4_squirrel_NW_003943632.1:1221  TTGACCTAGAAGTGCAGTGGA
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3_owl_NW_018510867.1:4449643-4  ttttc-tttttttagaggca
4_squirrel_NW_003943632.1:4195  ttttctttttttttagaggca
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3_owl_NW_018510867.1:4449642-4  tttttc-ttttttttagaggc
4_squirrel_NW_003943632.1:4195  tttttctttttttttagaggc
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3_owl_NW_018509268.1:456957-45  cacctgggccaacacggtgaa
4_squirrel_NW_003943646.1:1502  caccctggccaacatggtgaa
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3_owl_NW_018504164.1:2735066-2  tcttttcacctcTCAGTGTCT
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4_squirrel_NW_003943646.1:9503  caggcagatctcgaggtcaag
Spacer
0_Test_loci_CMOS_chr1:12318704  ttcaaatattttgtattaaCT
1_cebus_NW_016107377.1:6798103  NNNNNATATTTTGTATTAACT
2_marmoset_NC_013896.1:1231870  ttcaaatattttgtattaaCT
3_owl_NW_018510867.1:1757948-1  ttcaaatattttgtattaact
4_squirrel_NW_003943632.1:6792  ttcaaatattttatattaact
Spacer
0_Test_loci_CMOS_chr1:13194634  TTCTCAGGTTCTCCTGAGGAC
1_cebus_NW_016107377.1:5966208  TTCTCAGGTTCTCCTGAGGGC
2_marmoset_NC_013896.1:1319463  TTCTCAGGTTCTCCTGAGGAC
3_owl_NW_018510867.1:938736-93  TTCTCAGGTTCTCCTGAGGGC
4_squirrel_NW_003943632.1:7612  TTCTCAGgttctcctgagggc
Spacer
0_Test_loci_CMOS_chr1:27268200  cctgtagtcccagctactcag
1_cebus_NW_016107329.1:1020309  cctgtagtcccagctactcgg
2_marmoset_NC_013896.1:2726820  cctgtagtcccagctactcag
3_owl_NW_018510819.1:1096308-1  cctgtagtcccagctactcgg
4_squirrel_NW_003943632.1:2093  NNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_CMOS_chr1:54627261  AAAGTCCTATGTAATCCCTTC
1_cebus_NW_016107429.1:3650472  TAAGTCCTATGTAATCCCTTC
2_marmoset_NC_013896.1:5462726  AAAGTCCTATGTAATCCCTTC
3_owl_NW_018509268.1:13535416-  TAAGTCCTATGTAATCCCTTC
4_squirrel_NW_003943625.1:8845  TAAGTCCTATGTAATCCCTTC
Spacer
0_Test_loci_CMOS_chr1:58607516  ATaactaaatattctaaaata
1_cebus_NW_016107376.1:1159682  ATaactaaatattctaaaata
2_marmoset_NC_013896.1:5860751  ATaactaaatattctaaaata
3_owl_NW_018487996.1:3450606-3  ATaactaaatattctaaaata
4_squirrel_NW_003943625.1:5169  ATaactaaatattctaaaata
Spacer
0_Test_loci_CMOS_chr1:62195522  gttggctatttttaaagttat
1_cebus_NW_016107768.1:546960-  GTTGGCTATTTTTAAGGTTAT
2_marmoset_NC_013896.1:6219552  gttggctatttttaaagttat
3_owl_NW_018503287.1:3071246-3  GTTGGCTATTTTTAAGGTTAT
4_squirrel_NW_003943625.1:1933  gttggctatttttaaggttat
Spacer
0_Test_loci_CMOS_chr1:65019954  atgttaaataattcattttca
1_cebus_NW_016107409.1:1282563  atgttaaataattcattttca
2_marmoset_NC_013896.1:6501995  atgttaaataattcattttca
3_owl_NW_018503287.1:355489-35  gtgttaaataattcattttca
```

```
4_squirrel_NW_003943760.1:3140  ATGT----TAATTCATTTTCA
Spacer
0_Test_loci_CMOS_chr1:65177442  NNNNNNNNNNNNNNNNNNNNN
1_cebus_NW_016107409.1:1431172  ---------------------
2_marmoset_NC_013896.1:6517744  NNNNNNNNNNNNNNNNNNNNN
3_owl_NW_018503287.1:208419-20  ---------------------
4_squirrel_NW_003943760.1:2990  ---------------------
Spacer
0_Test_loci_MOS_chr1:9490161-9  AGAGCTCTACAAATTACCAAG
1_cebus_NW_016107473.1:3224311  AGGGCTCTACAAATTACCTGG
2_marmoset_NC_013896.1:9490161  AGAGCTCTACAAATTACCAAG
3_owl_NW_018510867.1:4543709-4  ATGGCTCTACAAATTACCTAG
4_squirrel_NW_003943632.1:4092  AGGGCTCTACAAATTACCTGG
Spacer
0_Test_loci_MOS_chr1:25541777-  ACTATGATCCTATAACTGAAA
1_cebus_NW_016107329.1:8503005  GCTATGATCCTATAACTG-AA
2_marmoset_NC_013896.1:2554177  ACTATGATCCTATAACTGAAA
3_owl_NW_018510822.1:362428-36  GCTATGATCCTATAACTG-AA
4_squirrel_NW_003943632.1:1930  GCTATGATCCTATAACTG-AA
Spacer
0_Test_loci_MOS_chr1:28568306-  AAGGCCTGTGAC--TGACTGT
1_cebus_NW_016107329.1:1149910  AAGGCTTGTGACTATGACTGT
2_marmoset_NC_013896.1:2856830  AAGGCCTGTGAC--TGACTGT
3_owl_NW_018510861.1:918615-92  AAGGCTTGTGACTCTGACTGT
4_squirrel_NW_003943632.1:2216  AAGGCTTGTGACTATGACAGC
Spacer
0_Test_loci_MOS_chr1:28713288-  aggcaaaatacCAACGTCCAG
1_cebus_NW_016108088.1:136137-  aggcaaaataccAACGTCCAG
2_marmoset_NC_013896.1:2871328  aggcaaaatacCAACGTCCAG
3_owl_NW_018510872.1:17809-189  aggcaaaatgcCAACGTCCAG
4_squirrel_NW_003943632.1:2229  aggcaaaataccACTGTCCAG
Spacer
0_Test_loci_MOS_chr1:41685266-  aacctcctgagtagctgggac
1_cebus_NW_016107344.1:8426742  --------------------
2_marmoset_NC_013896.1:4168526  aacctcctgagtagctgggac
3_owl_NW_018509268.1:1275945-1  aacctcctgagtagctgggac
4_squirrel_NW_003943646.1:1580  aacctcctgagtagctgggac
Spacer
0_Test_loci_MOS_chr1:42959313-  GAAAGGAAGTAACACAAGAGG
1_cebus_NW_016107344.1:7252656  gaaaagaaGCAACACAAGAGG
2_marmoset_NC_013896.1:4295931  GAAAGGAAGTAACACAAGAGG
3_owl_NW_018509268.1:2475014-2  gaaaGGAAGCAACACAAGAGG
4_squirrel_NW_003943646.1:1698  GAAAGGAAGCAGCACAAGAGG
Spacer
0_Test_loci_S_chr2:45570181-45  GGCACGGTATGGATATCATTG
1_cebus_NW_016107654.1:70350-7  GGTACGGTATGGATATCATAG
2_marmoset_NW_003188012.1:705-  GACATGGTATGGATATCATAG
3_owl_NW_018503287.1:442721-44  GGCACGGTATGGATATCATAG
4_squirrel_NW_003943760.1:3217  GGCACGGTATGGATATCATAG
Spacer
0_Test_loci_S_chr4:13456984-13  ---------------------
1_cebus_NW_016107336.1:2233047  ---------------------
2_marmoset_NC_013899.1:1345698  ---------------------
3_owl_NW_018506177.1:3059930-3  ---------------------
4_squirrel_NW_003943626.1:1134  aagcctgtaatNNNNNNNNNN
Spacer
0_Test_loci_S_chr5:86832791-86  ---------------------
1_cebus_NW_016107436.1:3928124  ---------------------
2_marmoset_NC_013900.1:8683279  ---------------------
3_owl_NW_018503376.1:2493992-2  ---------------------
4_squirrel_NW_003943636.1:2178  NNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_S_chr8:8294494-829  ---------------------
```

```
1_cebus_NW_016107664.1:1674958  cttgacctagtgatctacccg
2_marmoset_NC_013903.1:8294494  ---------------------
3_owl_NW_018508315.1:9466304-9  ---------------------
4_squirrel_NW_003943644.1:6949  cttgacctcgtgatccaccca
Spacer
0_Test_loci_S_chr22:9476401-94  ---------------------
1_cebus_NW_016107578.1:776237-  ---------------------
2_marmoset_NC_013917.1:9476401  ---------------------
3_owl_NW_018505408.1:9025252-9  ---------------------
4_squirrel_NW_003943712.1:6908  NNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_S_chr22:42782083-4  ---------------------
1_cebus_NW_016107788.1:422597-  ---------------------
2_marmoset_NC_013917.1:4278208  ---------------------
3_owl_NW_018512065.1:1285741-1  ---------------------
4_squirrel_NW_003943731.1:5979  NNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_S_chr5:86832791-86  ---------------------
1_cebus_NW_016107436.1:3928124  ---------------------
2_marmoset_NC_013900.1:8683279  ---------------------
3_owl_NW_018503376.1:2493992-2  ---------------------
4_squirrel_NW_003943636.1:2178  NNNNNNNNNNNNNNNNNNNN
Spacer
0_Test_loci_S_chr8:8294494-829  ---------------------
1_cebus_NW_016107664.1:1674958  ---------------------
2_marmoset_NC_013903.1:8294494  ---------------------
3_owl_NW_018508315.1:9466304-9  ---------------------
4_squirrel_NW_003943644.1:6949  ctctcgacctcgtgatccacc
Spacer
0_Test_loci_S_chr22:9476401-94  ---------------------
1_cebus_NW_016107578.1:776237-  ---------------------
2_marmoset_NC_013917.1:9476401  ---------------------
3_owl_NW_018505408.1:9025252-9  NNNNNNNNNNNNNNNNNNNN
4_squirrel_NW_003943712.1:6908  ---------------------
Spacer
0_Test_loci_OS_chr1:5927621-59  TTTACAGAAATTTCTGGAagt
1_cebus_NW_016107652.1:2289429  TTTGCAGAAATTTCCGGAagt
2_marmoset_NC_013896.1:5927621  TTTACAGAAATTTCTGGAagt
3_owl_NW_018510891.1:3120270-3  TTTGCAGAAATTTCTGGAAGT
4_squirrel_NW_003943632.1:6539  TTTGCAGAAATTTCCAGAAGt
Spacer
0_Test_loci_OS_chr1:12507317-1  ctcaggaggctgaggcaggag
1_cebus_NW_016107377.1:6612567  cttgggaggctgaggcaggag
2_marmoset_NC_013896.1:1250731  ctcaggaggctgaggcaggag
3_owl_NW_018510867.1:1572769-1  cttgggaggctgaggcaggag
4_squirrel_NW_003943632.1:6979  cttgggaggctgaggcaggag
Spacer
0_Test_loci_OS_chr1:13374123-1  G--------------------
1_cebus_NW_016107377.1:5796932  GTATAAATGATATAGAATAAA
2_marmoset_NC_013896.1:1337412  G--------------------
3_owl_NW_018510867.1:772859-77  G--------------------
4_squirrel_NW_003943632.1:7785  G--------------------
Spacer
0_Test_loci_OS_chr1:14733162-1  ---------------------
1_cebus_NW_016107627.1:856244-  ---------------------
2_marmoset_NC_013896.1:1473316  ---------------------
3_owl_NW_018505863.1:10394603-  ---------------------
4_squirrel_NW_003943632.1:9065  aggcgggcggatcacgaggtc
Spacer
0_Test_loci_OS_chr1:15561995-1  gcttcaagcgatcctcctgcc
1_cebus_NW_016107627.1:1682694  gcttcaagcaatcctcctgcc
2_marmoset_NC_013896.1:1556199  gcttcaagcgatcctcctgcc
3_owl_NW_018505863.1:9585936-9  gcttcaagcgatcctcctgcc
```

```
4_squirrel_NW_003943632.1:9904  gcttcaagtgatcctcctgcc
Spacer
0_Test_loci_OS_chr1:23747323-2  tccttttctctgtgtgcaca
1_cebus_NW_016107329.1:6820747  tccttttctctgtgtgtaca
2_marmoset_NC_013896.1:2374732  tccttttctctgtgtgcaca
3_owl_NW_018505863.1:1690211-1  TCCTTTTTCTCTGTGCGCACA
4_squirrel_NW_003943632.1:1764  TCCTTTTTCTCTGTGTGCACA
Spacer
0_Test_loci_OS_chr1:28326258-2  TTAGCCA-GAAGCCCTTG---
1_cebus_NW_016107329.1:1126533  TTGGCCAGGAAGCCCTTG---
2_marmoset_NC_013896.1:2832625  TTAGCCA-GAAGCCCTTG---
3_owl_NW_018510819.1:8293-9407  TTA-CCAGGAAGCCCTGGTAA
4_squirrel_NW_003943632.1:2194  TTAGCCAGGAAGCCCTTG---
Spacer
0_Test_loci_OS_chr1:28568307-2  AAAGGCCTGTGAC--TGACTG
1_cebus_NW_016107329.1:1149910  AAAGGCTTGTGACTATGACTG
2_marmoset_NC_013896.1:2856830  AAAGGCCTGTGAC--TGACTG
3_owl_NW_018510861.1:918615-92  AAAGGCTTGTGACTCTGACTG
4_squirrel_NW_003943632.1:2216  AAAGGCTTGTGACTATGACAG
Spacer
0_Test_loci_OS_chr1:29483707-2  caagaccagcctggccagcat
1_cebus_NW_016108018.1:448879-  caagaccagtctggccagcat
2_marmoset_NC_013896.1:2948370  caagaccagcctggccagcat
3_owl_NW_018510816.1:124750-12  caagaccagcctggccagcat
4_squirrel_NW_003943632.1:2300  caagaccagcctggtcagcat
Spacer
```

Figure A3.1: Alignment of randomly selected polyDetect output using dataset DS1, marmoset as the reference genome, and *Alu*Ta15 as the repeat sequence. The extracted sequence from the reference marmoset genome polyDetect output coordinates the contains the word, "Test" with the cooresponding letters indicating which genomes share that insertion (See Table 3.1). Individual alignments are separated by "Spacer" sequence. Note: the alignments depicted here are nucleotides 500-1000 from each alignment for easier viewing. As such, some longer alignments may be truncated. Dashes in the alignment indicate a gap.

Table A3.5: Capuchin monkey genotype based on PCR results of lineage-specific, polymorphic *Alu* elements. " 0 0" indicates a homozygous absent band, "1 0" indicates a heterozygous insertion, and "1 1" indicates a homozygous present insertion.

#	325		351		360		471		806		860		1173	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	-9	-9	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	-9	-9	1	1	1	1	1	1	1	1	1	1
7	1	1	-9	-9	1	1	1	1	1	1	1	1	1	1
8	1	1	-9	-9	1	1	1	1	1	1	1	1	1	1
9	1	1	-9	-9	1	1	1	1	1	1	1	1	1	0
10	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	-9	-9	0	0	0	0	0	0	-9	-9	-9	-9	0	0
18	0	0	0	0	0	0	0	0	-9	-9	-9	-9	0	0

#	1366		1371		1404		1487		1494		1551		1697	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	-9	-9	-9	-9	-9	-9	0	0	-9	-9	-9	-9
8	1	1	-9	-9	-9	-9	-9	-9	0	0	-9	-9	1	1
9	1	0	-9	-9	0	0	1	0	0	0	1	1	1	1
10	1	0	1	1	0	0	1	1	0	0	1	1	1	1
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0

18	0	0	0	0	0	0	0	0	0	0	0	0

#	1848		2131		2355		2461		2591		2599	
1	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	-9	-9	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1
8	1	0	0	0	1	1	1	1	1	1	1	1
9	0	0	0	0	1	0	1	1	1	1	1	1
10	0	0	1	1	1	1	1	1	1	1	1	1
11	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0	0

#	2608		2711		2732		2854		2855		3125		3463	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	-9	-9
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	0	0	1	1	1	1	0	0	1	1
8	1	1	1	1	0	0	1	1	1	1	0	0	1	1
9	1	1	1	1	0	0	1	1	1	1	0	0	1	1
10	1	1	1	1	0	0	1	1	1	1	0	0	1	1
11	0	0	1	1	0	0	0	0	0	0	0	0	0	0
12	0	0	1	1	0	0	0	0	0	0	0	0	0	0
13	0	0	1	1	0	0	0	0	0	0	0	0	0	0
14	0	0	1	1	0	0	0	0	0	0	0	0	0	0
15	0	0	1	1	0	0	0	0	0	0	0	0	0	0
16	0	0	1	1	0	0	0	0	0	0	0	0	0	0
17	0	0	1	1	0	0	0	0	0	0	0	0	0	0
18	0	0	1	1	0	0	0	0	0	0	0	0	0	0

#	4058		4534		4904		5070		5091		5205		5259	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	-9	-9
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	1	1	1	1	1	0	1	1	1	1	1	1	1	0
10	1	1	1	1	1	1	1	1	1	1	-9	-9	1	1
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0

#	5584		5693		5662		5800		5824		5860	
1	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0
5	1	1	1	1	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1	1	1	1	1
9	1	0	1	1	1	0	1	0	1	1	1	0
10	1	1	1	1	1	1	1	1	1	1	1	1
11	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	-9	-9

Table A3.5 Key

#	Species	Common name	Origin	ID
1	Homo sapiens	Human	ATCC	Hela CCL-2
2	Callithrix jacchus	Common marmoset	NERPRC	cj393-99, A02-738
3	Saimiri s. sciureus	Common Squirrel monkey	SDFZ	KB4544
4	Aotus trivirgatus	Three-striped Owl monkey	ATCC	CRL1556
5	Cebus imitator	White-faced sapajou (Ref) (untufted)	Wash U.	Cc_AM_T3
6	Cebus capucinus	White-faced sapajou (untufted)	FMNH	UF 31995
7	Cebus capucinus	White-faced sapajou (untufted)	FMNH	UF 32380
8	Cebus albifrons	White-fronted capuchin monkey (untufted)	Chris C. Conroy	MVZ:Mamm:193675
9	Cebus albifrons	White-fronted capuchin monkey (untufted)	Chris C. Conroy	MVZ:Mamm:193676
10	Cebus albifrons albifrons	White-fronted capuchin monkey (untufted)	SDZICR	KB 4207
11	Sapajus appella	Tufted capuchin monkey	LSUMZ	LSUMZ M-6112
12	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46592
13	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46594
14	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46595
15	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46596
16	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46597
17	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46598
18	Sapajus appella	Tufted capuchin monkey	Dr. Link Olson	UAM 46599

Table A3.6: Owl monkey genotype based on PCR results of polymorphic lineage-specific *Alu* insertions. The header numbers refer to primer numbers. " 0 0" indicates a homozygous absent band, "1 0" indicates a heterozygous insertion, and "1 1" indicates a homozygous present insertion.

#	622		827		887		1120		1446		1620		1780	
1	0	0	0	0	-9	-9	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	1	1	1	1	1	1	1	1	0	1	1	0	1	1
9	1	1	1	1	1	1	1	1	0	0	1	0	1	1
10	1	1	1	1	1	1	1	1	0	1	1	0	1	1
11	1	1	1	1	1	1	1	1	0	1	1	1	1	1
12	1	1	1	1	1	1	1	1	0	1	1	1	1	1
13	1	1	1	1	1	1	1	1	0	0	1	0	1	1
14	1	1	1	1	1	1	1	1	0	1	1	1	1	1
15	1	1	1	1	1	1	1	1	0	0	1	1	1	1
16	1	1	1	1	1	1	1	1	0	0	1	1	1	0
17	1	0	0	0	-9	-9	0	0	-9	-9	0	0	0	0
18	1	1	0	0	-9	-9	0	0	0	0	0	0	0	0
19	1	0	-9	-9	-9	-9	0	0	0	0	0	0	0	0
20	1	0	-9	-9	-9	-9	0	0	0	0	0	0	0	0
21	1	0	0	0	-9	-9	0	0	0	0	0	0	0	0
22	1	0	-9	-9	-9	-9	0	0	0	0	0	0	0	0
23	1	1	1	1	1	1	1	1	0	0	0	0	0	0
24	1	1	1	1	1	1	1	1	0	0	0	0	0	0
25	1	1	1	1	1	1	1	1	0	0	0	0	0	0
26	0	0	1	0	1	1	0	0	0	0	0	0	0	0

#	1834		1898		2188		2845		2897		3097		3424	
1	0	0	0	0	0	0	0	0	-9	-9	-9	-9	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
5	0	0	1	1	0	0	0	0	0	0	0	0	1	1
6	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
7	0	0	1	1	0	0	0	0	0	0	0	0	0	0
8	1	1	1	1	1	0	1	0	1	0	1	0	1	1
9	1	1	1	1	0	0	1	1	0	0	0	0	1	1
10	1	0	1	1	0	0	1	1	1	0	1	0	1	1
11	1	1	1	1	0	0	1	1	0	0	1	0	1	1
12	1	1	1	1	1	0	1	0	1	0	1	0	1	1
13	1	1	1	1	0	0	1	1	0	0	0	0	1	1
14	1	0	1	1	1	0	1	0	0	0	0	0	1	1
15	0	0	1	1	0	0	1	1	0	0	0	0	1	1
16	1	1	1	1	0	0	1	1	0	0	0	0	1	1
17	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
18	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
19	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
20	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
21	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
22	0	0	1	1	0	0	0	0	0	0	0	0	-9	-9
23	0	0	1	1	0	0	0	0	0	0	0	0	1	1
24	0	0	1	1	0	0	0	0	0	0	0	0	1	1
25	0	0	-9	-9	0	0	0	0	0	0	0	0	1	0
26	0	0	1	0	0	0	0	0	0	0	0	0	1	1

#	3581		3908		4723		4922		6430	
1	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0
3	0	0	-9	-9	0	0	0	0	0	0
4	-9	-9	1	1	1	1	0	0	0	0
5	-9	-9	1	1	1	1	0	0	0	0
6	-9	-9	1	1	1	1	0	0	0	0
7	-9	-9	1	1	1	1	0	0	0	0
8	1	1	1	1	1	1	1	1	1	0
9	1	1	1	1	1	1	1	0	1	0
10	1	1	1	1	1	1	1	1	0	0
11	1	1	1	1	1	1	1	1	1	0
12	1	1	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1	1	0
15	1	1	1	1	1	1	1	1	1	0
16	-9	-9	1	1	1	1	1	1	1	1
17	1	1	-9	-9	1	1	0	0	0	0
18	-9	-9	-9	-9	1	1	0	0	0	0
19	1	1	1	1	1	1	0	0	0	0
20	1	1	-9	-9	1	1	0	0	0	0
21	1	1	-9	-9	1	1	0	0	0	0
22	1	1	-9	-9	1	1	0	0	0	0
23	-9	-9	1	1	1	1	0	0	1	1
24	1	1	1	1	1	1	0	0	1	1
25	-9	-9	-9	-9	-9	-9	0	0	1	1
26	-9	-9	-9	-9	1	0	0	0	0	0

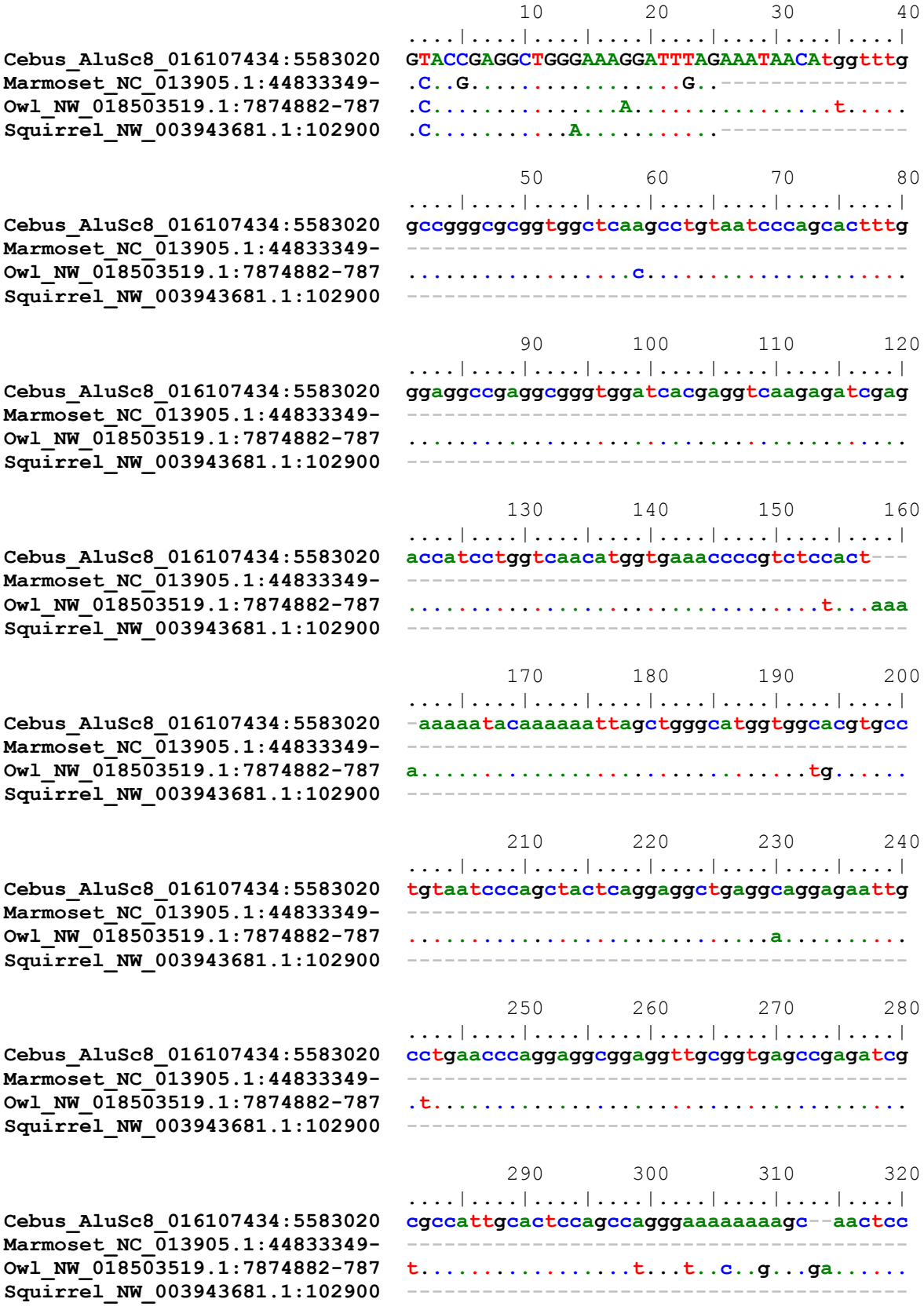
Table A3.6 Key

#	Species	Common name	Origin	ID
1	*Homo sapiens*	Human	ATCC	HeLa CCL-2
2	*Callithrix jacchus*	Common marmoset	NERPRC	cj393-99, A02-738
3	*Saimiri boliviensis*	Bolivian squirrel monkey	KCCMR	2514
4	*Aotus trivirgatus*	Three-striped owl monkey	ATCC	CRL1556
5	*Aotus trivirgatus*	Three-striped owl monkey	MSB	MSB:Mamm:212080
6	*Aotus trivirgatus*	Three-striped owl monkey	MSB	MSB:Mamm:41436
7	*Aotus trivirgatus*	Three-striped owl monkey	MSB	MSB:Mamm:56874
8	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85464
9	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85676
10	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	86116
11	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	86334
12	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85835
13	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85974
14	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	86224
15	*Aotus nancymaae*	Nancy Ma's night monkey	SDZICR	KB9129
16	*Aotus nancymaae*	Nancy Ma's night monkey	KCCMR	85841
17	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	Chris C. Conroy	MVZ Mamm 153564
18	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	Chris C. Conroy	MVZ Mamm 155159
19	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	86100
20	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	86218
21	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	85962
22	*Aotus vociferans*	Noisy owl monkey (Spix's night monkey)	KCCMR	86230
23	*Aotus azarae*	Azara's night monkey (southern night monkey)	KCCMR	85457
24	*Aotus azarae*	Azara's night monkey (southern night monkey)	KCCMR	85818
25	*Aotus azarae*	Azara's night monkey (southern night monkey)	SDZICR	KB10043
26	*Aotus lemurinus griseimembra*	Panamanian night monkey	SDZICR	KB4883

Table A4.1: Shared *Alu* insertion primers

Name	Forward oligonucleotide (5'-3')	Reverse oligonucleotide (5'-3')
CM_blat_1	GTCTTcGGgTTGTTTTGGTG	CTCTGCCCTGAAGTCACAAAG
CM_blat_2	TGcGTTATTTGATGCCCTTG	GCCAAaGGAGTAAGAGGTCAG
CM_blat_3	tCCTCTAAGTAGACTCGCTCTTG	GAcGATGGGCCTTTAaCCTTG
CM_blat_4	ATGATCCCCTTCTCCCTTTCG	GAGAACATGTGCCCAGGATG
CM_blat_5	ACACTGCTGGCTTCACATTAC	CACCAAACAGGAAAGTACTCC
CMO_blat_1	AGGgGTGGCAATGGTTAAAAC	AACACTCCCAGGGAAGGTAAC
CMO_blat_2	GCACAACAGCAAGCATTACG	AGGAtGCAGGAGAGAAGTTGG
CMO_blat_3	GAGCACAAGTGCATggaaata	AGCCAGCTGTCCACATTTCT
CMO_blat_4	TTGTTCTTCCGTAGCTTTCTTC	ACTGGAGAATTTGGCAGTCCC
CMO_blat_5	TGCCATTTTCTTCGAGATGGC	ACTACCATGCCCaacaaaatg
CMS_blat_1	TGCAACCATCTCTCTCTTAG	TGTGGCTGCCTGAAGAACTAT
CMS_blat_2	AGtCCAGCTGCCACTCATATG	GTGAGTGGGCATGTGAAAGAG
CMS_blat_3	GGCTCTCAGTGGTCTATTTTCTG	TCTGCTGATTCTGGGAAGGT
CMS_blat_4	acaatgcctggaatGTAGCTG	TAGTTTaGACAGGGGCCCTTG
CMS_blat_5	TGTTTGCACTGCACTGTTCAT	tgtgTTCACCTTAGAAGCCTCA
CO_blat_1	CCCTTACACCATACTGCTTGG	TGTGCCTCTGATCTTTCTTTTG
CO_blat_2	TGCTGGCTACCTGTTCTTCAT	tttccattttctgggTGAGAC
CO_blat_3	AGGCTGCCTTTGATCTCATTA	CAGCACCCAGTGCTCTGTATAA
CO_blat_4	GCAGAAATCCTGGTGAACTG	TGTTTATCAGGTGCCTACTTTG
COS_blat_1	CTGCCTCATCCAAGCTTACC	GCAAAACAAGCCTTTTAACTgc
COS_blat_2	TCCACTCTGACTTTTGGGAAAG	GCTGCTTTGACTGGCATAACT
COS_blat_3	GCAAGAGCTACAAAGTAACACACA	ccaaataccacatgttcccatt
COS_blat_4	TGTTCACTGggttcattcactt	CAAGTCAATAAGGCCAGCTCA
COS_blat_5	gtttggATTGCTGTAGGTTTG	GATAGTACTGGAAATTCTAGCCAG
CS_blat_1	CTTATGATCCTGCCATTTCCA	TCTTGATGGGGAGGCACTGC
CS_blat_2	TCAGATGGATTCTAGGGTGCT	GTGCAAATCCCAAAATGGTAG
CS_blat_3	ATCTGGGAAGCAGACACACAA	TTCATGGAAAGCAGGtttcag
CS_blat_4	CCCTCCTCCTTAGAATGGACA	GGACTGCAGAGGGTAAGGAC
CS_blat_5	tccagGAGTCCCTGCTAATAAA	gactagcctcaaattcctgagc
MO_blat_1	CTGAGGACAAAGATGCAATGAC	AGAGGAACCTTTGTCgGATTAG
MO_blat_2	TGTGGCAGAGATCACAACTTG	aGGACAGACTTTCCTTGATG
MO_blat_3	TTACgGAcACCCACAAATAGC	CCTAGTGCTTTcCTTCCTGTTG
MO_blat_4	TCCACCAAAGGCAAATCACAG	TCAGGGCACTAATTGAAAGGG
MO_blat_5	TTCCCGTTAGCAGAAAATCAG	GCAAGGTGTACTCAAAGCATTC
MOS_blat_1	GCTTTGCAGTTtGTGTCAAGG	TTAGGGGACAGTGGTACTTGG
MOS_blat_2	TAAGTGTCACTGGGGAACTGG	GGGGCCAGCATATAAAAGGTG
MOS_blat_3	AAACCTGTGATCTAAAGCAGTATACC	GGAGTCTATTGAGTGCCTAGGG
MOS_blat_4	TCAAGCCTGccataatttcaa	ACCTCATTCATAAAGCCTCCA
MOS_blat_5	GATACAGCACTCAGGAACCAG	GCAgTTAACCATCACACCAAC

MS_blat_1	GAGTGGCAGACAACAACCAAG	ACTTGACTCCTAGCTCACTCC
MS_blat_3	TCACAAAGTCCTGCCATTCTG	TTGGTGTAGAAAGCCCAGGAG
MS_blat_4	TGTGTATGTGTGGAGGAGTTCT	TCTGTTCAGCTTGCCTCATC
MS_blat_5	CAACCCCAAGACTGAaTACCC	TGGAGCTGGAGAGAGTTCAAG
OS_blat_1	TTGTATCTGTGGTTCCCCATC	aatccacagatgctcaagtcc
OS_blat_2	TGGTAACAGAGCTGGATTCTGA	ACCTTGGTTGCAACTTCATCA
OS_blat_3	CAGACTGTGGTCACACAATACA	TGTCAGATCCTTACTGCTGgtt
OS_blat_4	caaggctgcaggtaactgtg	AAGGCGAGTCATATTGTTTGC
OS_blat_5	ATCGCTCTGGTTGCTGTATTG	CCTCATTACGTGGCAGACACT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Marmoset_NC_013905.1:44833349- .C..G.....G..----------
Owl_NW_018503519.1:7874882-787 .C.....A.....t.....
Squirrel_NW_003943681.1:102900 .C.....A.....----------
50 60 70 80
Cebus_AluSc8_016107434:5583020 gccgggcgcggtggctcaagcctgtaatcccagcactttg
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 .....c.....
Squirrel_NW_003943681.1:102900 ----------
90 100 110 120
Cebus_AluSc8_016107434:5583020 ggaggccgaggcgggtggatcacgaggtcaagagatcgag
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 .....
Squirrel_NW_003943681.1:102900 ----------
130 140 150 160
Cebus_AluSc8_016107434:5583020 accatcctggtcaacatggtgaaaccccgtctccact---
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 .....t...aaa
Squirrel_NW_003943681.1:102900 ----------
170 180 190 200
Cebus_AluSc8_016107434:5583020 -aaaaatacaaaaaattagctgggcatggtggcacgtgcc
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 a.....tg.....
Squirrel_NW_003943681.1:102900 ----------
210 220 230 240
Cebus_AluSc8_016107434:5583020 tgtaatcccagctactcaggaggctgaggcaggagaattg
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 .....a.....
Squirrel_NW_003943681.1:102900 ----------
250 260 270 280
Cebus_AluSc8_016107434:5583020 cctgaacccaggaggcggaggttgcggtgagccgagatcg
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 .t.....
Squirrel_NW_003943681.1:102900 ----------
290 300 310 320
Cebus_AluSc8_016107434:5583020 cgccattgcactccagccagggaaaaaaaagc--aactcc
Marmoset_NC_013905.1:44833349- ----------
Owl_NW_018503519.1:7874882-787 t.....t...t..c..g...ga.....
Squirrel_NW_003943681.1:102900 ----------

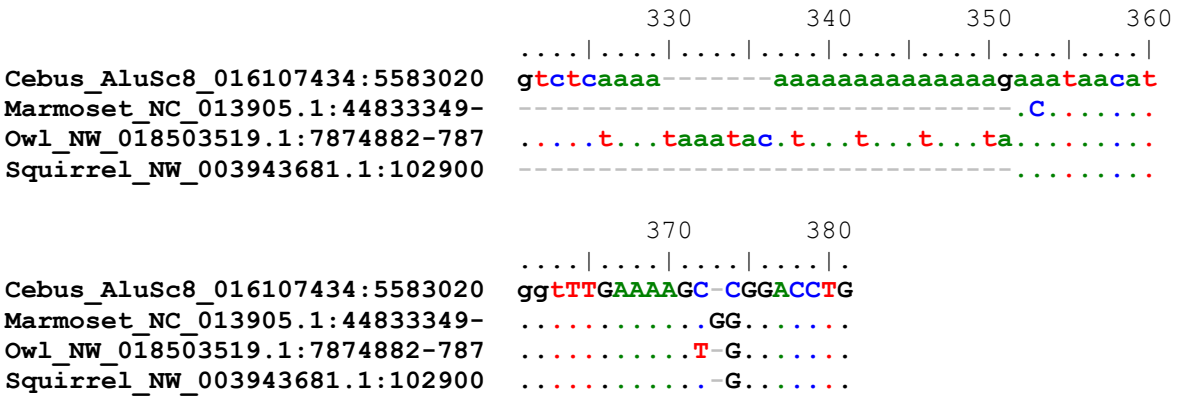


Figure A4.1: Sample Alignment of shared *Alu* locus. An *Alu* element ascertained from the capuchin monkey genome was aligned to the marmoset, owl monkey and squirrel monkey genomes and the orthologous sequences extracted and aligned via MUSCLE. This sample alignment indicates that this *Alu* element is shared among the capuchin monkey and owl monkey genomes to the exclusion of marmoset and squirrel monkey genomes. Shown here is a slice of the full alignment to show only some flanking sequence and the presence or absence of the *Alu* element. Dots represent a shared nucleotide while diagnostic substitutions are shown as the corrected base compared to the capuchin monkey sequence. Note that the capuchin monkey and owl monkey shared *Alu* insertion share the same TSD.

Table A4.2: RepeatMasker ouptput of 189 *Alu* subfamilies. *See key

1*	2*	3*	4*	5*	6*	7*	8*	9*	10*	11*	12*	13*	14*	15*
2811	0	0	0	AluJb	1	312	0	+	AluJb	SINE/Alu	1	312	0	1
2464	1.4	0	0.3	sf24	1	289	0	+	AluJb	SINE/Alu	1	288	-24	38
2436	1.7	0	0.3	sf9	1	289	0	+	AluJb	SINE/Alu	1	288	-24	106
2439	2.1	0	0	sf87	1	288	0	+	AluJb	SINE/Alu	1	288	-24	103
2415	2.1	0	0.3	sf88	1	289	0	+	AluJb	SINE/Alu	1	288	-24	104
2433	2.1	0	0.3	sf22	1	289	0	+	AluJb	SINE/Alu	1	288	-24	36
2445	2.1	0	0	sf78	1	288	0	+	AluJb	SINE/Alu	1	288	-24	93
2386	2.4	0	0.3	sf92	1	289	0	+	AluJb	SINE/Alu	1	288	-24	109
2430	2.4	0	0	sf56	2	288	0	+	AluJb	SINE/Alu	2	288	-24	70
2821	0	0	0	AluJo	1	312	0	+	AluJo	SINE/Alu	1	312	0	2
2531	1	0	0.3	sf21	1	289	0	+	AluJo	SINE/Alu	1	288	-24	35
2452	1.4	0	0.3	sf2	1	289	0	+	AluJo	SINE/Alu	1	288	-24	34
2418	1.7	0.3	0	sf57	1	287	0	+	AluJo	SINE/Alu	1	288	-24	71
2421	2.8	0	0	sf89	1	288	0	+	AluJo	SINE/Alu	1	288	-24	105
2823	0	0	0	AluJr	1	312	0	+	AluJr	SINE/Alu	1	312	0	3
2530	0.3	0	0.3	sf40	1	289	0	+	AluJr	SINE/Alu	1	288	-24	54
2545	0.3	0	0.3	sf70	1	289	0	+	AluJr	SINE/Alu	1	288	-24	85
2529	0.7	0	0.3	sf67	1	289	0	+	AluJr	SINE/Alu	1	288	-24	81
2511	0.7	0	0.3	sf79	1	289	0	+	AluJr	SINE/Alu	1	288	-24	94
2515	1	0	0.3	sf83	1	289	0	+	AluJr	SINE/Alu	1	288	-24	99
2444	1.7	0	0.3	sf23	1	289	0	+	AluJr	SINE/Alu	1	288	-24	37
2428	1.7	0	0.3	sf45	1	289	0	+	AluJr	SINE/Alu	1	288	-24	59
2405	1.7	0	0.7	sf58	1	290	0	+	AluJr	SINE/Alu	1	288	-24	72
2421	2.1	0	0.3	sf41	1	289	0	+	AluJr	SINE/Alu	1	288	-24	55
2437	2.1	0	0.3	sf68	1	289	0	+	AluJr	SINE/Alu	1	288	-24	82
2829	0.3	0	0	AluJr4	1	312	0	+	AluJr4	SINE/Alu	1	312	0	4
2826	0	0	0	AluSp	1	313	0	+	AluSp	SINE/Alu	1	313	0	11
2542	0.7	0.3	0	sf15_31	1	288	0	+	AluSp	SINE/Alu	1	289	-24	29
2518	1	0.3	0	sf72	1	288	0	+	AluSp	SINE/Alu	1	289	-24	87
2826	0	0	0	AluSq	1	313	0	+	AluSq	SINE/Alu	1	313	0	12
2574	0.3	0	0	sf32	1	289	0	+	AluSq	SINE/Alu	1	289	-24	45
2835	0	0	0	AluSq10	1	313	0	+	AluSq10	SINE/Alu	1	313	0	13
2831	0	0	0	AluSq2	1	313	0	+	AluSq2	SINE/Alu	1	313	0	14
2576	0.3	0	0	sf80	1	289	0	+	AluSq2	SINE/Alu	1	289	-24	96
2554	0.7	0	0	sf16	1	289	0	+	AluSq2	SINE/Alu	1	289	-24	30

2554	0.7	0	0	sf29	1	289	0	+	AluSq2	SINE/Alu	1	289	-24	42
2530	1	0	0.3	sf14	1	290	0	+	AluSq2	SINE/Alu	1	289	-24	28
2551	1.4	0	0	sf33	1	289	0	+	AluSq2	SINE/Alu	1	289	-24	46
2804	0	0	0	AluSq4	1	311	0	+	AluSq4	SINE/Alu	1	311	0	15
2792	0	0	0	AluSg	1	310	0	+	AluSg	SINE/Alu	1	310	0	8
2495	2.1	0	0	sf34	1	286	0	+	AluSg	SINE/Alu	1	286	-24	47
2408	3.8	0	0.3	sf18	1	287	0	+	AluSg	SINE/Alu	1	286	-24	32
2405	3.9	0	0	subfam 20_JB	1	280	0	+	AluSg	SINE/Alu	1	280	-30	135
2370	5	0	0	subfam 22_Owl	1	280	0	+	AluSg	SINE/Alu	2	281	-29	140
2789	0	0	0	AluSg4	1	310	0	+	AluSg4	SINE/Alu	1	310	0	9
2384	3.9	0	0	subfam 4_Owl	1	280	0	+	AluSg4	SINE/Alu	2	281	-29	176
2362	4.6	0	0	subfam 3_JB	1	280	0	+	AluSg4	SINE/Alu	1	280	-30	166
2796	0	0	0	AluSg7	1	309	0	+	AluSg7	SINE/Alu	1	309	0	10
2542	0.3	0	0	sf17	1	285	0	+	AluSg7	SINE/Alu	1	285	-24	31
2542	0.3	0	0	sf55	1	285	0	+	AluSg7	SINE/Alu	1	285	-24	69
2815	0	0	0	AluSx	1	312	0	+	AluSx	SINE/Alu	1	312	0	16
2548	0.3	0	0	sf93	1	288	0	+	AluSx	SINE/Alu	1	288	-24	110
2558	0.3	0	0	sf26	1	288	0	+	AluSx	SINE/Alu	1	288	-24	40
2574	0.3	0	0	sf30	1	288	0	+	AluSx	SINE/Alu	1	288	-24	44
2558	0.3	0	0	sf75	1	288	0	+	AluSx	SINE/Alu	1	288	-24	90
2544	1	0	0	sf8	1	288	0	+	AluSx	SINE/Alu	1	288	-24	95
2814	0	0	0	AluSx1	1	312	0	+	AluSx1	SINE/Alu	1	312	0	17
2570	0.3	0	0	sf59	1	288	0	+	AluSx1	SINE/Alu	1	288	-24	73
2473	2.1	0.3	0	sf19	1	287	0	+	AluSx1	SINE/Alu	1	288	-24	33
2472	2.4	0	0	sf48	1	288	0	+	AluSx1	SINE/Alu	1	288	-24	62
2799	0	0	0	AluSx3	1	311	0	+	AluSx3	SINE/Alu	1	311	0	18
2483	1.4	0	0	sf91	1	287	0	+	AluSx3	SINE/Alu	1	287	-24	108
2798	0	0	0	AluSx4	1	310	0	+	AluSx4	SINE/Alu	1	310	0	19
2821	0	0	0	AluSz	1	312	0	+	AluSz	SINE/Alu	1	312	0	20
2552	0.3	0	0	sf77	2	288	0	+	AluSz	SINE/Alu	2	288	-24	92
2496	2.8	0	0	sf7	2	288	0	+	AluSz	SINE/Alu	2	288	-24	84
2818	0	0	0	AluSz6	1	312	0	+	AluSz6	SINE/Alu	1	312	0	21
2538	0.7	0	0	sf25	1	288	0	+	AluSz6	SINE/Alu	1	288	-24	39
2557	0.7	0	0	sf28	1	288	0	+	AluSz6	SINE/Alu	1	288	-24	41
2550	1	0	0	sf50	1	288	0	+	AluSz6	SINE/Alu	1	288	-24	64
2787	0	0	0	AluSc	1	309	0	+	AluSc	SINE/Alu	1	309	0	5
2483	0.3	0	0.3	sf90	1	286	0	+	AluSc	SINE/Alu	1	285	-24	107
2520	0.3	0	0.3	sf3	1	286	0	+	AluSc	SINE/Alu	1	285	-24	43

2520	0.3	0	0.3	sf54	1	286	0	+	AluSc	SINE/Alu	1	285	-24	68
2535	0.3	0	0	sf64	1	285	0	+	AluSc	SINE/Alu	1	285	-24	78
2495	0.7	0	0.3	sf81	1	286	0	+	AluSc	SINE/Alu	1	285	-24	97
2400	1.4	0	0.7	sf84	1	287	0	+	AluSc	SINE/Alu	1	285	-24	100
2449	2.1	0	0	subfam 1_Ceb	1	279	0	+	AluSc	SINE/Alu	2	280	-29	132
2432	2.1	0	0	subfam 1_Owl	1	279	0	+	AluSc	SINE/Alu	2	280	-29	134
2341	2.9	1.1	0	subfam 35_JB	1	276	0	+	AluSc	SINE/Alu	1	279	-30	160
2422	3.2	0	0	subfam 8_JB	1	279	0	+	AluSc	SINE/Alu	1	279	-30	186
2394	3.2	0	0	subfam 7_Ceb	1	279	0	+	AluSc	SINE/Alu	2	280	-29	182
2417	3.5	0	0.3	sf12	1	286	0	+	AluSc	SINE/Alu	1	285	-24	27
2321	3.6	1.1	0	subfam 6_Ceb	1	277	0	+	AluSc	SINE/Alu	1	280	-29	180
2268	3.6	1.1	1.1	subfam 7_Owl	1	280	0	+	AluSc	SINE/Alu	1	280	-29	184
2312	3.6	1.1	0	subfam 21_Owl	1	276	0	+	AluSc	SINE/Alu	2	280	-29	138
2315	3.6	1.1	0	subfam 14_Owl	1	274	0	+	AluSc	SINE/Alu	4	280	-29	121
2375	3.9	0	0	subfam 28_JB	1	279	0	+	AluSc	SINE/Alu	1	279	-30	150
2358	3.9	0	0	subfam 13_Owl	1	279	0	+	AluSc	SINE/Alu	2	280	-29	119
2325	4	0.4	0	subfam 38_JB	1	278	0	+	AluSc	SINE/Alu	1	279	-30	163
2343	4.7	0	0	subfam 5_Owl	1	279	0	+	AluSc	SINE/Alu	2	280	-29	179
2317	5	0	0.4	subfam 26_Owl	1	281	0	+	AluSc	SINE/Alu	1	280	-29	148
2321	5	0	0	subfam 12_Owl	1	279	0	+	AluSc	SINE/Alu	2	280	-29	117
2806	0	0	0	AluSc5	1	309	0	+	AluSc5	SINE/Alu	1	309	0	6
2802	0	0	0	AluSc8	1	311	0	+	AluSc8	SINE/Alu	1	311	0	7
2520	1.1	0	0	sf35	1	287	0	+	AluSc8	SINE/Alu	1	287	-24	48
2655	0	0	0	AluTa7	1	294	0	+	AluTa7	SINE/Alu	1	294	0	24
2567	0.7	0.3	0	sf74	1	293	0	+	AluTa7	SINE/Alu	1	294	0	89
2612	0.3	0	0	AluTa10	1	287	0	+	AluTa10	SINE/Alu	1	287	0	22
2538	0.4	0	0	subfam 1_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	133
2547	0.4	0	0	subfam 3_Owl	1	281	0	+	AluTa10	SINE/Alu	2	282	-5	167
2516	0.7	0	0	subfam 21_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	137
2510	0.7	0	0	subfam 22_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	139

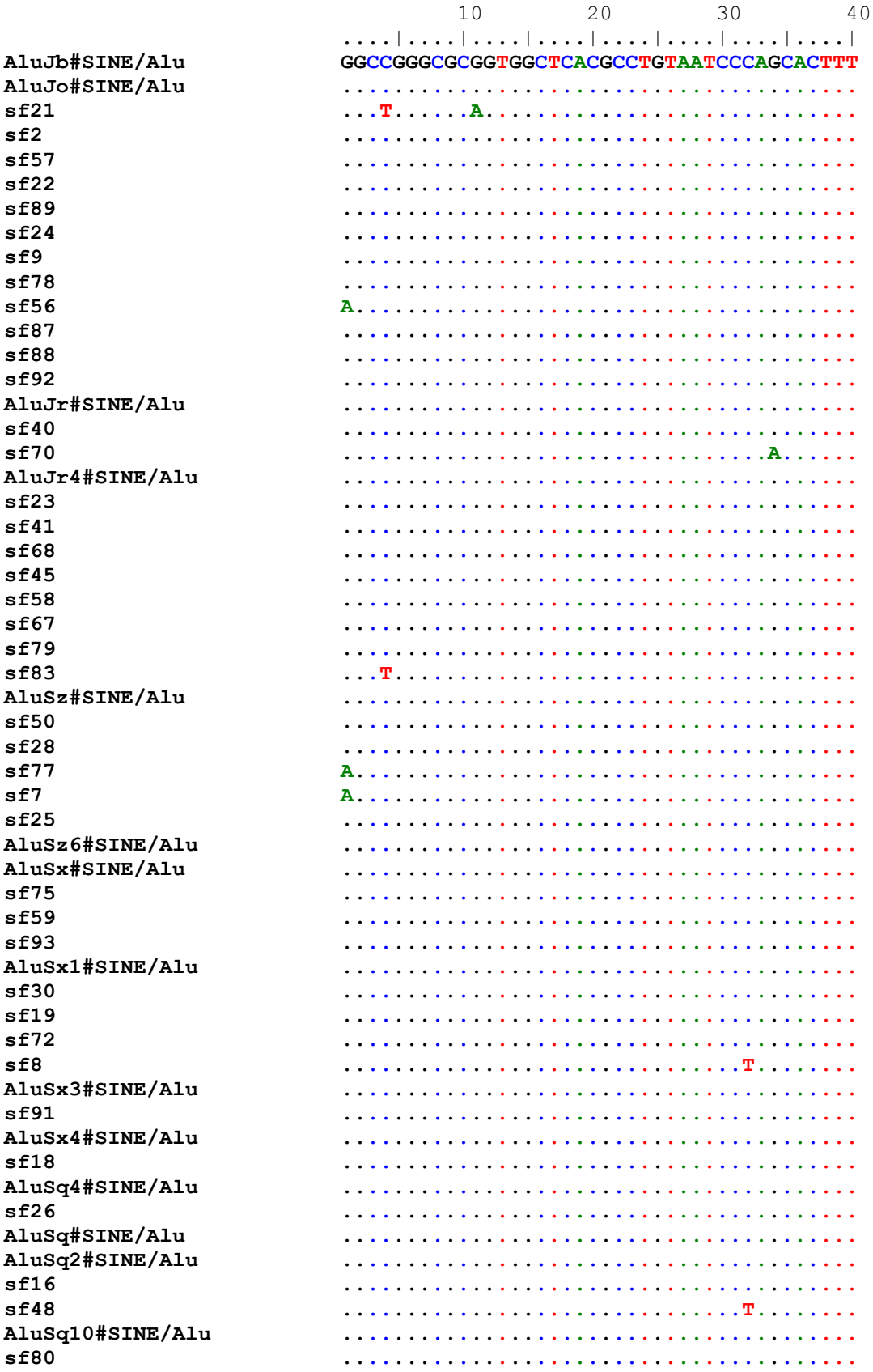
2516	0.7	0	0	subfam 23_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	14 1
2529	0.7	0	0	subfam 33_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	15 8
2562	0.7	0	0	sf10	1	287	0	+	AluTa10	SINE/Alu	1	287	0	25
2563	0.7	0	0	sf69	1	287	0	+	AluTa10	SINE/Alu	1	287	0	83
2518	0.7	0	0	subfam 15_Owl	1	281	0	+	AluTa10	SINE/Alu	2	282	-5	12 3
2538	0.7	0	0	subfam 16_Owl	1	281	0	+	AluTa10	SINE/Alu	2	282	-5	12 5
2478	0.7	0	1.1	subfam 29_Owl	1	284	0	+	AluTa10	SINE/Alu	2	282	-5	15 2
2507	1.1	0	0	subfam 25_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	14 5
2511	1.1	0	0	subfam 34_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	15 9
2514	1.1	0	0	subfam 40_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	16 8
2525	1.1	0	0	subfam 6_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	18 1
2532	1.1	0	0	sf39	2	287	0	+	AluTa10	SINE/Alu	2	287	0	52
2471	1.4	0	0	subfam 9_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	18 8
2488	1.4	0	0	subfam 8_Owl	1	281	0	+	AluTa10	SINE/Alu	2	282	-5	18 7
2389	1.8	1.1	0	subfam 11_JB	1	278	0	+	AluTa10	SINE/Alu	1	281	-6	11 4
2490	1.8	0	0	subfam 42_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	17 0
2457	1.8	0	0.3	subfam 11_Owl	1	283	0	+	AluTa10	SINE/Alu	1	282	-5	11 5
2480	2.1	0	0	subfam 17_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	12 6
2441	2.1	0	0	subfam 26_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	14 7
2484	2.1	0	0	subfam 45_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	17 3
2389	2.2	0.4	0	subfam 41_JB	1	278	0	+	AluTa10	SINE/Alu	1	279	-8	16 9
2457	2.5	0	0	subfam 31_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	15 6
2422	2.9	0	0	subfam 7_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	18 3
2469	3.1	0	0	sf61	1	287	0	+	AluTa10	SINE/Alu	1	287	0	75
2414	3.2	0	0	subfam 27_JB	1	281	0	+	AluTa10	SINE/Alu	1	281	-6	14 9
2371	3.2	0.4	0	subfam 44_JB	1	280	0	+	AluTa10	SINE/Alu	1	281	-6	17 2
2430	3.2	0	0	subfam 3_Ceb	1	281	0	+	AluTa10	SINE/Alu	2	282	-5	16 5
2365	4.3	0	0	subfam 5_Ceb	1	281	0	+	AluTa10	SINE/Alu	2	282	-5	17 7

2635	0	0	0	AluTa15	1	288	0	+	AluTa15	SINE/Alu	1	288	0	23
2628	0	0	0	sf44	2	288	0	+	AluTa15	SINE/Alu	2	288	0	58
2552	0.3	0	0	subfam 0_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	111
2602	0.3	0	0	sf85	1	288	0	+	AluTa15	SINE/Alu	1	288	0	101
2598	0.3	0	0	sf86	1	288	0	+	AluTa15	SINE/Alu	1	288	0	102
2615	0.3	0	0	sf47	1	288	0	+	AluTa15	SINE/Alu	1	288	0	61
2602	0.3	0	0	sf63	1	288	0	+	AluTa15	SINE/Alu	1	288	0	77
2605	0.3	0	0	sf73	1	288	0	+	AluTa15	SINE/Alu	1	288	0	88
2608	0.3	0	0	sf76	1	288	0	+	AluTa15	SINE/Alu	1	288	0	91
2411	0.4	2.9	0	subfam 18_JB	1	274	0	+	AluTa15	SINE/Alu	1	282	-6	128
2512	0.4	0.4	0	subfam 24_JB	1	281	0	+	AluTa15	SINE/Alu	1	282	-6	143
2428	0.4	1.8	0	subfam 20_Owl	1	277	0	+	AluTa15	SINE/Alu	2	283	-5	136
2588	0.7	0	0	sf37	1	288	0	+	AluTa15	SINE/Alu	1	288	0	50
2575	0.7	0	0	sf38	1	288	0	+	AluTa15	SINE/Alu	1	288	0	51
2594	0.7	0	0	sf42	1	288	0	+	AluTa15	SINE/Alu	1	288	0	56
2544	0.7	0	1	sf46	1	291	0	+	AluTa15	SINE/Alu	1	288	0	60
2589	0.7	0	0	sf52	1	288	0	+	AluTa15	SINE/Alu	1	288	0	66
2591	0.7	0	0	sf53	1	288	0	+	AluTa15	SINE/Alu	1	288	0	67
2587	0.7	0	0	sf60	1	288	0	+	AluTa15	SINE/Alu	1	288	0	74
2589	0.7	0	0	sf62	1	288	0	+	AluTa15	SINE/Alu	1	288	0	76
2586	0.7	0	0	sf71	1	288	0	+	AluTa15	SINE/Alu	1	288	0	86
2589	0.7	0	0	sf82	1	288	0	+	AluTa15	SINE/Alu	1	288	0	98
2394	0.7	1.4	0.3	subfam 18_Owl	1	279	0	+	AluTa15	SINE/Alu	2	283	-5	129
2526	0.7	0	0	subfam 4_Ceb	1	282	0	+	AluTa15	SINE/Alu	2	283	-5	174
2582	0.7	0	0	sf66	2	288	0	+	AluTa15	SINE/Alu	2	288	0	80
2561	1	0	0	sf36	1	288	0	+	AluTa15	SINE/Alu	1	288	0	49
2532	1.1	0	0	subfam 10_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	112
2506	1.1	0	0	subfam 12_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	116
2449	1.1	0.4	0	subfam 19_JB	1	281	0	+	AluTa15	SINE/Alu	1	282	-6	130
2516	1.1	0	0	subfam 10_Owl	1	282	0	+	AluTa15	SINE/Alu	2	283	-5	113
2413	1.1	1.1	0.3	subfam 17_Owl	1	280	0	+	AluTa15	SINE/Alu	2	283	-5	127
2438	1.1	1.1	0	subfam 23_Owl	1	279	0	+	AluTa15	SINE/Alu	2	283	-5	142
2507	1.4	0	0	subfam 16_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	124

2510	1.4	0	0	subfam 29_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	15 1
2553	1.4	0	0	sf11	1	288	0	+	AluTa15	SINE/Alu	1	288	0	26
2515	1.4	0	0.3	sf4	1	289	0	+	AluTa15	SINE/Alu	1	288	0	53
2547	1.4	0	0	sf51	1	288	0	+	AluTa15	SINE/Alu	1	288	0	65
2424	1.4	1.1	0	subfam 25_Owl	1	279	0	+	AluTa15	SINE/Alu	2	283	-5	14 6
2495	1.8	0	0	subfam 2_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	15 4
2474	1.8	0	0	subfam 37_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	16 2
2482	1.8	0	0	subfam 5_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	17 8
2375	1.8	1.4	0	subfam 24_Owl	1	279	0	+	AluTa15	SINE/Alu	1	283	-5	14 4
2368	1.8	1.1	0.3	subfam 19_Owl	1	280	0	+	AluTa15	SINE/Alu	2	283	-5	13 1
2449	1.8	0	0	subfam 2_Ceb	1	282	0	+	AluTa15	SINE/Alu	2	283	-5	15 3
2485	2.1	0	0	subfam 14_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	12 0
2456	2.1	0	0	subfam 4_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	17 5
2367	2.1	1.1	0.3	subfam 9_Owl	1	281	0	+	AluTa15	SINE/Alu	1	283	-5	18 9
2496	2.1	0	0	sf65	1	288	0	+	AluTa15	SINE/Alu	1	288	0	79
2470	2.1	0	0	subfam 30_JB	1	281	0	+	AluTa15	SINE/Alu	2	282	-6	15 5
2422	2.1	0	0	subfam 8_Ceb	1	282	0	+	AluTa15	SINE/Alu	2	283	-5	18 5
2408	2.5	0.4	0	subfam 15_JB	1	281	0	+	AluTa15	SINE/Alu	1	282	-6	12 2
2447	2.5	0	0	subfam 39_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	16 4
2468	2.5	0	0	subfam 43_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	17 1
2408	2.8	0	0.3	subfam 36_JB	1	283	0	+	AluTa15	SINE/Alu	1	282	-6	16 1
2474	3.1	0	0	sf5	1	288	0	+	AluTa15	SINE/Alu	1	288	0	63
2390	3.2	0	0.3	subfam 32_JB	1	283	0	+	AluTa15	SINE/Alu	1	282	-6	15 7
2453	3.5	0	0	sf43	1	288	0	+	AluTa15	SINE/Alu	1	288	0	57
2309	6	0	0	subfam 13_JB	1	282	0	+	AluTa15	SINE/Alu	1	282	-6	11 8

Table A4.2 Key

Number	RepeatMasker output
1	Smith-Waterman Score
2	Percent divergence
3	Percent of deletion in the query sequence
4	Percent of insertions in the query sequence
5	Name of query sequence
6	Starting position of match in query sequence
7	Ending position of match in query sequence
8	Number of bases in query sequence past the ending position
9	Strand
10	Name of the matching interspersed repeat
11	Class of the repeat
12	Number of bases in the complement of repeat consensus sequence prior to the beginning of the match
13	Starting position of match in repeat consensus sequence
14	Ending position of match in repeat consensus sequence
15	Unique identifier for individual insertions


10
20
30
40
AluJb#SINE/Alu GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTT
AluJo#SINE/Alu
sf21
sf2
sf57
sf22
sf89
sf24
sf9
sf78
sf56
sf87
sf88
sf92
AluJr#SINE/Alu
sf40
sf70
AluJr4#SINE/Alu
sf23
sf41
sf68
sf45
sf58
sf67
sf79
sf83
AluSz#SINE/Alu
sf50
sf28
sf77
sf7
sf25
AluSz6#SINE/Alu
AluSx#SINE/Alu
sf75
sf59
sf93
AluSx1#SINE/Alu
sf30
sf19
sf72
sf8
AluSx3#SINE/Alu
sf91
AluSx4#SINE/Alu
sf18
AluSq4#SINE/Alu
sf26
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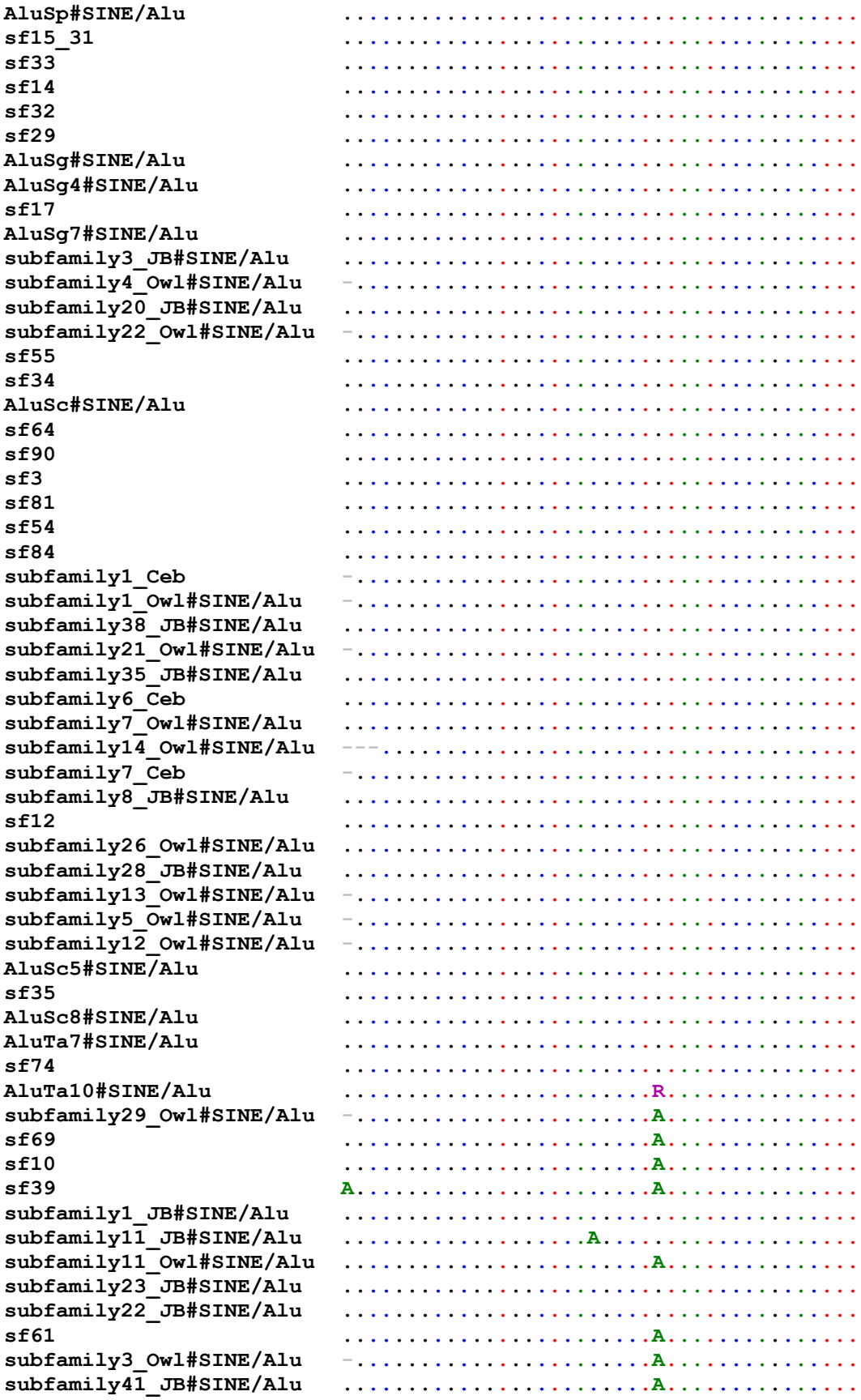
AluSq2#SINE/Alu
sf16
sf48
AluSq10#SINE/Alu
sf80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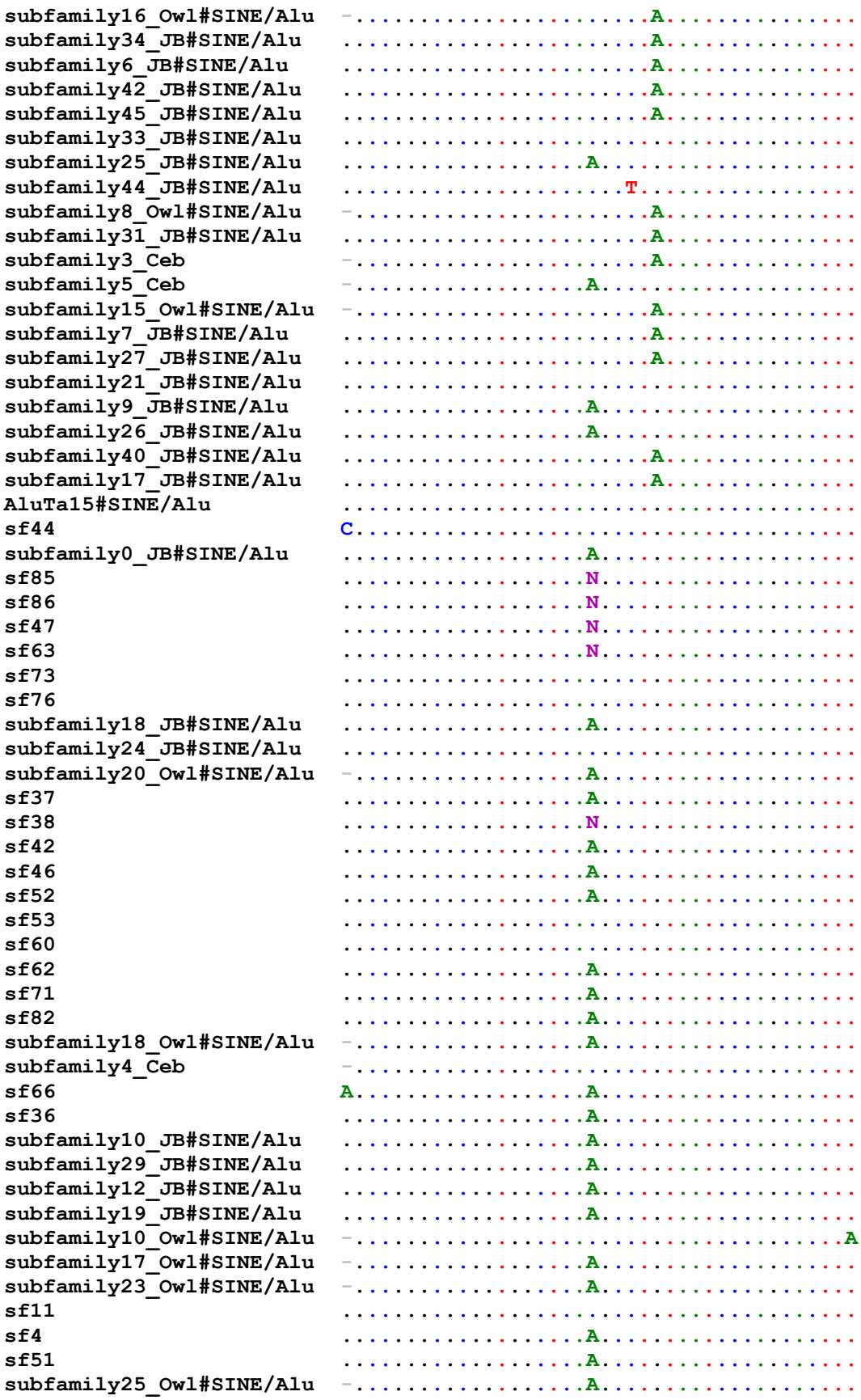
sf15_31
sf33
sf14
sf32
sf29
AluSg#SINE/Alu
AluSg4#SINE/Alu
sf17
AluSg7#SINE/Alu
subfamily3_JB#SINE/Alu
subfamily4_Owl#SINE/Alu
subfamily20_JB#SINE/Alu
subfamily22_Owl#SINE/Alu
sf55
sf34
AluSc#SINE/Alu
sf64
sf90
sf3
sf81
sf54
sf84
subfamily1_Ceb
subfamily1_Owl#SINE/Alu
subfamily38_JB#SINE/Alu
subfamily21_Owl#SINE/Alu
subfamily35_JB#SINE/Alu
subfamily6_Ceb
subfamily7_Owl#SINE/Alu
subfamily14_Owl#SINE/Alu
subfamily7_Ceb
subfamily8_JB#SINE/Alu
sf12
subfamily26_Owl#SINE/Alu
subfamily28_JB#SINE/Alu
subfamily13_Owl#SINE/Alu
subfamily5_Owl#SINE/Alu
subfamily12_Owl#SINE/Alu
AluSc5#SINE/Alu
sf35
AluSc8#SINE/Alu
AluTa7#SINE/Alu
sf74
AluTa10#SINE/Alu
subfamily29_Owl#SINE/Alu
sf69
sf10
sf39
subfamily1_JB#SINE/Alu
subfamily11_JB#SINE/Alu
subfamily11_Owl#SINE/Alu
subfamily23_JB#SINE/Alu
subfamily22_JB#SINE/Alu
sf61
subfamily3_Owl#SINE/Alu
subfamily41_JB#SINE/Alu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subfamily6_JB#SINE/Alu
subfamily42_JB#SINE/Alu
subfamily45_JB#SINE/Alu
subfamily33_JB#SINE/Alu
subfamily25_JB#SINE/Alu
subfamily44_JB#SINE/Alu
subfamily8_Owl#SINE/Alu
subfamily31_JB#SINE/Alu
subfamily3_Ceb
subfamily5_Ceb
subfamily15_Owl#SINE/Alu
subfamily7_JB#SINE/Alu
subfamily27_JB#SINE/Alu
subfamily21_JB#SINE/Alu
subfamily9_JB#SINE/Alu
subfamily26_JB#SINE/Alu
subfamily40_JB#SINE/Alu
subfamily17_JB#SINE/Alu
AluTa15#SINE/Alu
sf44
subfamily0_JB#SINE/Alu
sf85
sf86
sf47
sf63
sf73
sf76
subfamily18_JB#SINE/Alu
subfamily24_JB#SINE/Alu
subfamily20_Owl#SINE/Alu
sf37
sf38
sf42
sf46
sf52
sf53
sf60
sf62
sf71
sf82
subfamily18_Owl#SINE/Alu
subfamily4_Ceb
sf66
sf36
subfamily10_JB#SINE/Alu
subfamily29_JB#SINE/Alu
subfamily12_JB#SINE/Alu
subfamily19_JB#SINE/Alu
subfamily10_Owl#SINE/Alu
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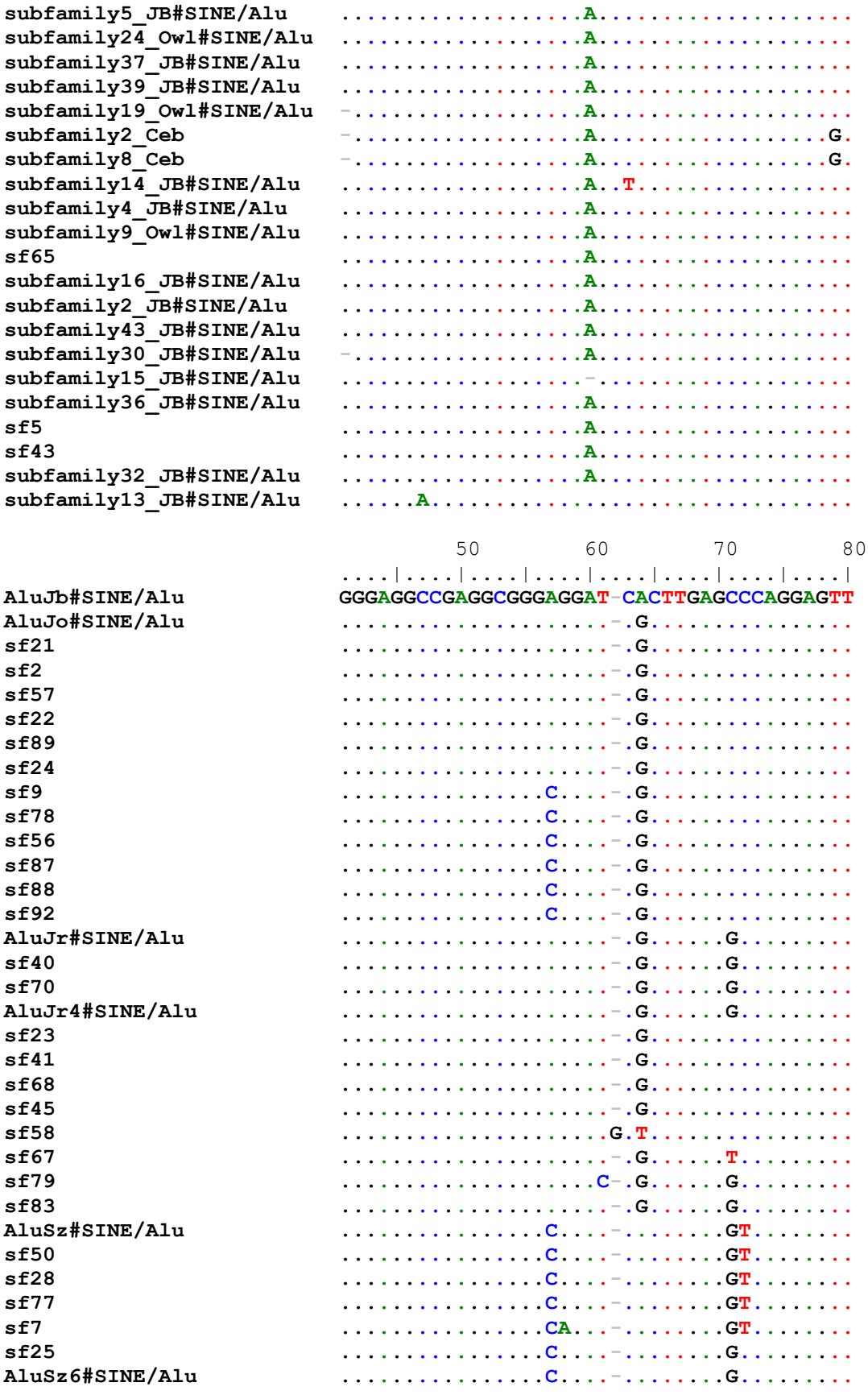
subfamily23_Owl#SINE/Alu
sf11
sf4
sf51
subfamily25_Owl#SINE/Alu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subfamily37_JB#SINE/Alu
subfamily39_JB#SINE/Alu
subfamily19_Owl#SINE/Alu
subfamily2_Ceb
subfamily8_Ceb
subfamily14_JB#SINE/Alu
subfamily4_JB#SINE/Alu
subfamily9_Owl#SINE/Alu
sf65
subfamily16_JB#SINE/Alu
subfamily2_JB#SINE/Alu
subfamily43_JB#SINE/Alu
subfamily30_JB#SINE/Alu
subfamily15_JB#SINE/Alu
subfamily36_JB#SINE/Alu
sf5
sf43
subfamily32_JB#SINE/Alu
subfamily13_JB#SINE/Alu
50
60
70
80
AluJb#SINE/Alu
GGGAGGCCGAGGCGGGAGGATCACTTGAGCCCAGGAGTT
AluJo#SINE/Alu
sf21
sf2
sf57
sf22
sf89
sf24
sf9
sf78
sf56
sf87
sf88
sf92
AluJr#SINE/Alu
sf40
sf70
AluJr4#SINE/Alu
sf23
sf41
sf68
sf45
sf58
sf67
sf79
sf83
AluSz#SINE/Alu
sf50
sf28
sf77
sf7
sf25
AluSz6#SINE/Alu

```
AluSx#SINE/Alu              ..............C....-...C....GT........
sf75                        ..............C....-...C....GT........
sf59                        ..............C....-...C....GT........
sf93                        ..............C....-...C....GT........
AluSx1#SINE/Alu             ..............C....-...C....GT........
sf30                        ..............C....-...C....GT........
sf19                        ..............C....-...C....GT........
sf72                        ..............C....-...C....GT.G......
sf8                         ..............C....-...C....GT........
AluSx3#SINE/Alu             ..............C....-.....--...GT........
sf91                        ..............C....-.....--...GT........
AluSx4#SINE/Alu             ..............C....-.....--...GT........
sf18                        ..............C....-.....--...GT........
AluSq4#SINE/Alu             ..............C....-.....--...GT........
sf26                        ..............C....-...C....GT........
AluSq#SINE/Alu              ..............C....-...C....GT........
AluSq2#SINE/Alu             ..............C....-...C....GT........
sf16                        ..............C....-...C....GT........
sf48                        ..............T....-...C....GT........
AluSq10#SINE/Alu            ..............T....-...C....GT........
sf80                        ..............C....-...C....GT........
AluSp#SINE/Alu              ..............C....-...C....GT.G......
sf15_31                     ..............C....-...C....GT.G......
sf33                        ..............C....-...C....GT........
sf14                        ..............C....-...C....GT........
sf32                        ..............C....-...C....GT........
sf29                        ..............C....-...C....GT........
AluSg#SINE/Alu              ..............C....-.....--...GT........
AluSg4#SINE/Alu             ..............T....-.....--...GT........
sf17                        ..............T....-.....--...GT........
AluSg7#SINE/Alu             ..............T....-.....--...GT........
subfamily3_JB#SINE/Alu      ..............T....-.....--A..GT........
subfamily4_Owl#SINE/Alu     ..............T....-.....--...GT........
subfamily20_JB#SINE/Alu     ..............C....-.....--A..GT........
subfamily22_Owl#SINE/Alu    ..............T....-.....--...GT........
sf55                        ..............T....-.....--...GT........
sf34                        ..............C....-.....--...GT........
AluSc#SINE/Alu              ..............C....-.....--...GT..A...A.
sf64                        ..............C....-.....--...GT..A...A.
sf90                        ..............C....-.....--...GT..C...A.
sf3                         ..............C....-.....--...GT..A...A.
sf81                        ..............C....-.....--...GT..A...AC
sf54                        ..............C....-.....--...GT..A...A.
sf84                        ..............C....-.....--...GT.CA...A.
subfamily1_Ceb              ..............T....-.....--...GT..A...A.
subfamily1_Owl#SINE/Alu     ..............C....-.....--...GT..A...A.
subfamily38_JB#SINE/Alu     ............A..T....-.....--...GT..A...A.
subfamily21_Owl#SINE/Alu    ..............C....-.....--...GT..A...A.
subfamily35_JB#SINE/Alu     ..............C....-.....--...GT..A...A.
subfamily6_Ceb              ..............C....-.....--...GT..A...A.
subfamily7_Owl#SINE/Alu     ..............C....-.....--...GT..A...A.
subfamily14_Owl#SINE/Alu    ............T...C....-.....--...GT..A...A.
subfamily7_Ceb              ..............C....-.....--...GT..A...A.
subfamily8_JB#SINE/Alu      ..............T....-.....--...GT..A...A.
sf12                        ..............C....-.....--...GT..A...A.
subfamily26_Owl#SINE/Alu    ..............C....-.....--...GT..A...A.
subfamily28_JB#SINE/Alu     ..............T....-.....--...GT..A...A.
```

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subfamily13_Owl#SINE/Alu  ..............C....-...--...GT..A...A.
subfamily5_Owl#SINE/Alu   ..............C....-...--...GT..A...A.
subfamily12_Owl#SINE/Alu  ..............C....-...--...GT..A...A.
AluSc5#SINE/Alu           ..............C....-...--...GT......A.
sf35                      ..............C....-...--...GT......A.
AluSc8#SINE/Alu           ..............C....-...--...GT......A.
AluTa7#SINE/Alu           ..............C....-...--...GT..A...A.
sf74                      ..............C....-...--...GT..A...A.
AluTa10#SINE/Alu          ..............T....-...--...GT..A...A.
subfamily29_Owl#SINE/Alu  ..............T....-...--...GT..A...A.
sf69                      ..............T....-...--...GT..A...A.
sf10                      ..............T....-...--...GT..A...A.
sf39                      ..............T....-...--...GT..A...A.
subfamily1_JB#SINE/Alu    ..............T....-...--...GT..A...A.
subfamily11_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily11_Owl#SINE/Alu  ..............T....-...--...GT..A...A.
subfamily23_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily22_JB#SINE/Alu   ..............T....-...--...GT..A...A.
sf61                      ..............T....-...--...GT..A...A.
subfamily3_Owl#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily41_JB#SINE/Alu   ..........A....T....-...--...GT..A...A.
subfamily16_Owl#SINE/Alu  ..........A....T....-...--...GT..A...A.
subfamily34_JB#SINE/Alu   ..........A....T....-...--...GT..A...A.
subfamily6_JB#SINE/Alu    ..........A....T....-...--...GT..A...A.
subfamily42_JB#SINE/Alu   ..........A....T....-...--...GT..A...A.
subfamily45_JB#SINE/Alu   .......T...A....T....-...--...GT..A...A.
subfamily33_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily25_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily44_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily8_Owl#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily31_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily3_Ceb            ..............T....-...--...GT..A...A.
subfamily5_Ceb            ..............T....-...--...GT..A...A.
subfamily15_Owl#SINE/Alu  ..............T....-...--...GT..A...A.
subfamily7_JB#SINE/Alu    ..............T....-...--...GT..A...A.
subfamily27_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily21_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily9_JB#SINE/Alu    ..............T....-...--...GT..A...A.
subfamily26_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily40_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily17_JB#SINE/Alu   ..............T....-...--...GT..A...A.
AluTa15#SINE/Alu          ..............T....-...--...GT..A...A.
sf44                      ..............T....-...--...GT..A...A.
subfamily0_JB#SINE/Alu    ..............T....-...--...GT..A...A.
sf85                      ..............T....-...--...GT..A..CA.
sf86                      ..............T....-...--...GT..A...A.
sf47                      ..............T....-...--...GT..A...A.
sf63                      ..............T....-...--...GT..A...A.
sf73                      ..............T....-...--...GT..A...A.
sf76                      ..............T....-...--...GT..A...A.
subfamily18_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily24_JB#SINE/Alu   ..............T....-...--...GT..A...A.
subfamily20_Owl#SINE/Alu  ..............T....-...--...GT..A...A.
sf37                      ..............T....-...--...GT..AC..A.
sf38                      ..............T....-...--...GT..A...A.
sf42                      ..............T....-...--...GT..A..TA.
sf46                      ..............T....-...--...GT..A...A.
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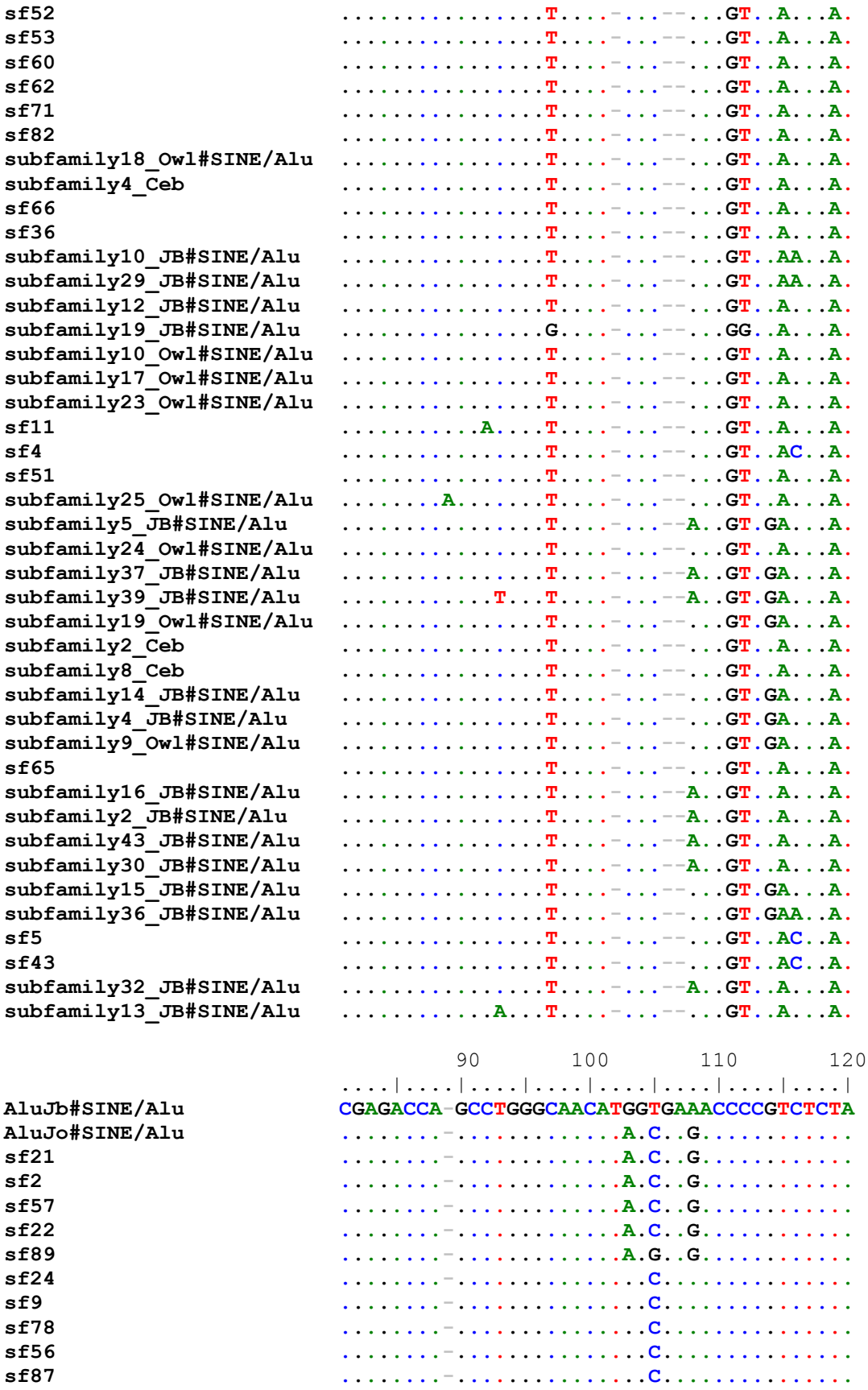
sf52
sf53
sf60
sf62
sf71
sf82
subfamily18_Owl#SINE/Alu
subfamily4_Ceb
sf66
sf36
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subfamily29_JB#SINE/Alu
subfamily12_JB#SINE/Alu
subfamily19_JB#SINE/Alu
subfamily10_Owl#SINE/Alu
subfamily17_Owl#SINE/Alu
subfamily23_Owl#SINE/Alu
sf11
sf4
sf51
subfamily25_Owl#SINE/Alu
subfamily5_JB#SINE/Alu
subfamily24_Owl#SINE/Alu
subfamily37_JB#SINE/Alu
subfamily39_JB#SINE/Alu
subfamily19_Owl#SINE/Alu
subfamily2_Ceb
subfamily8_Ceb
subfamily14_JB#SINE/Alu
subfamily4_JB#SINE/Alu
subfamily9_Owl#SINE/Alu
sf65
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subfamily2_JB#SINE/Alu
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subfamily30_JB#SINE/Alu
subfamily15_JB#SINE/Alu
subfamily36_JB#SINE/Alu
sf5
sf43
subfamily32_JB#SINE/Alu
subfamily13_JB#SINE/Alu
90
100
110
120
AluJb#SINE/Alu
CGAGACCA-GCCTGGGCAACATGGTGAAACCCCGTCTCTA
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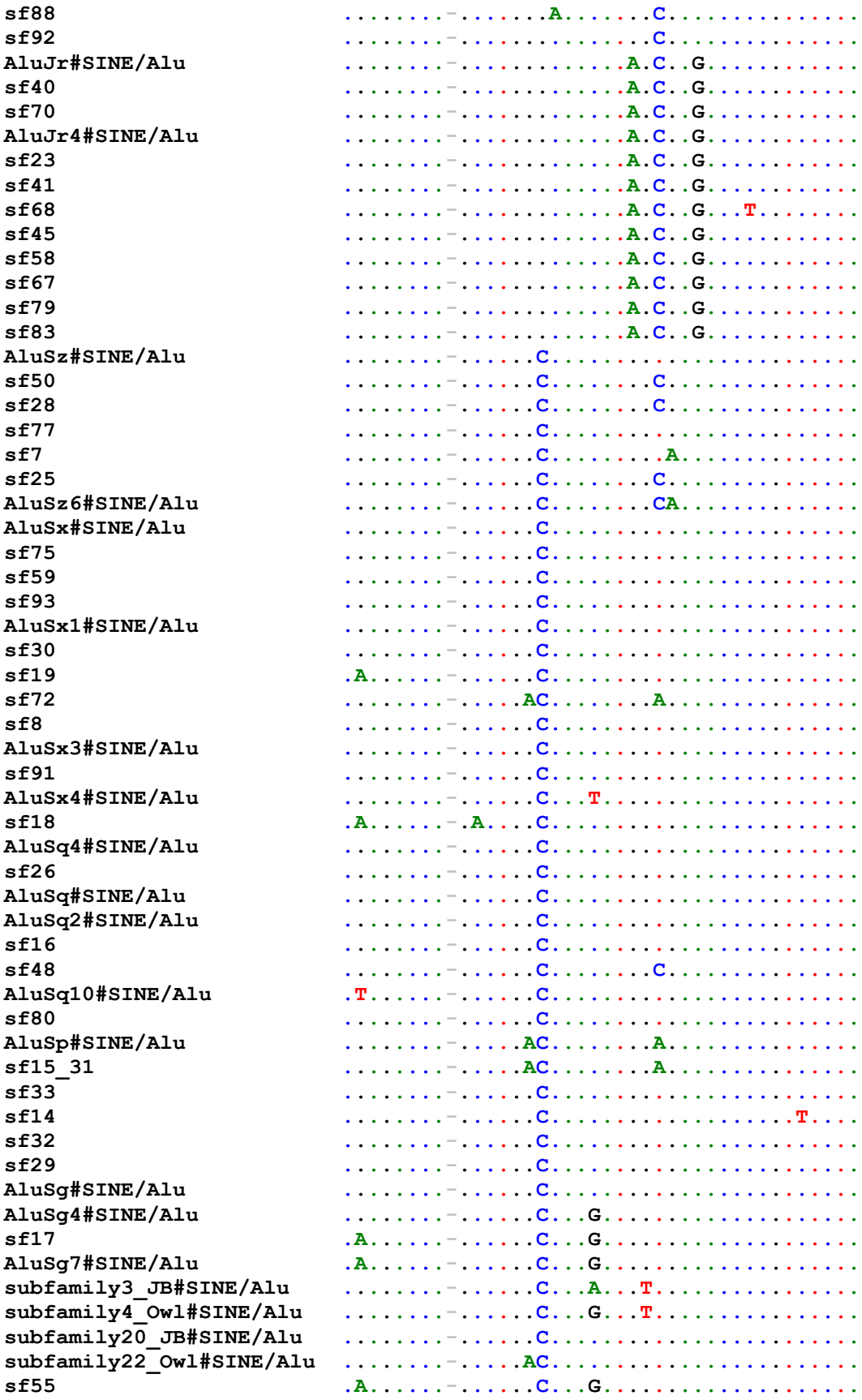
sf88
sf92
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sf40
sf70
AluJr4#SINE/Alu
sf23
sf41
sf68
sf45
sf58
sf67
sf79
sf83
AluSz#SINE/Alu
sf50
sf28
sf77
sf7
sf25
AluSz6#SINE/Alu
AluSx#SINE/Alu
sf75
sf59
sf93
AluSx1#SINE/Alu
sf30
sf19
sf72
sf8
AluSx3#SINE/Alu
sf91
AluSx4#SINE/Alu
sf18
AluSq4#SINE/Alu
sf26
AluSq#SINE/Alu
AluSq2#SINE/Alu
sf16
sf48
AluSq10#SINE/Alu
sf80
AluSp#SINE/Alu
sf15_31
sf33
sf14
sf32
sf29
AluSg#SINE/Alu
AluSg4#SINE/Alu
sf17
AluSg7#SINE/Alu
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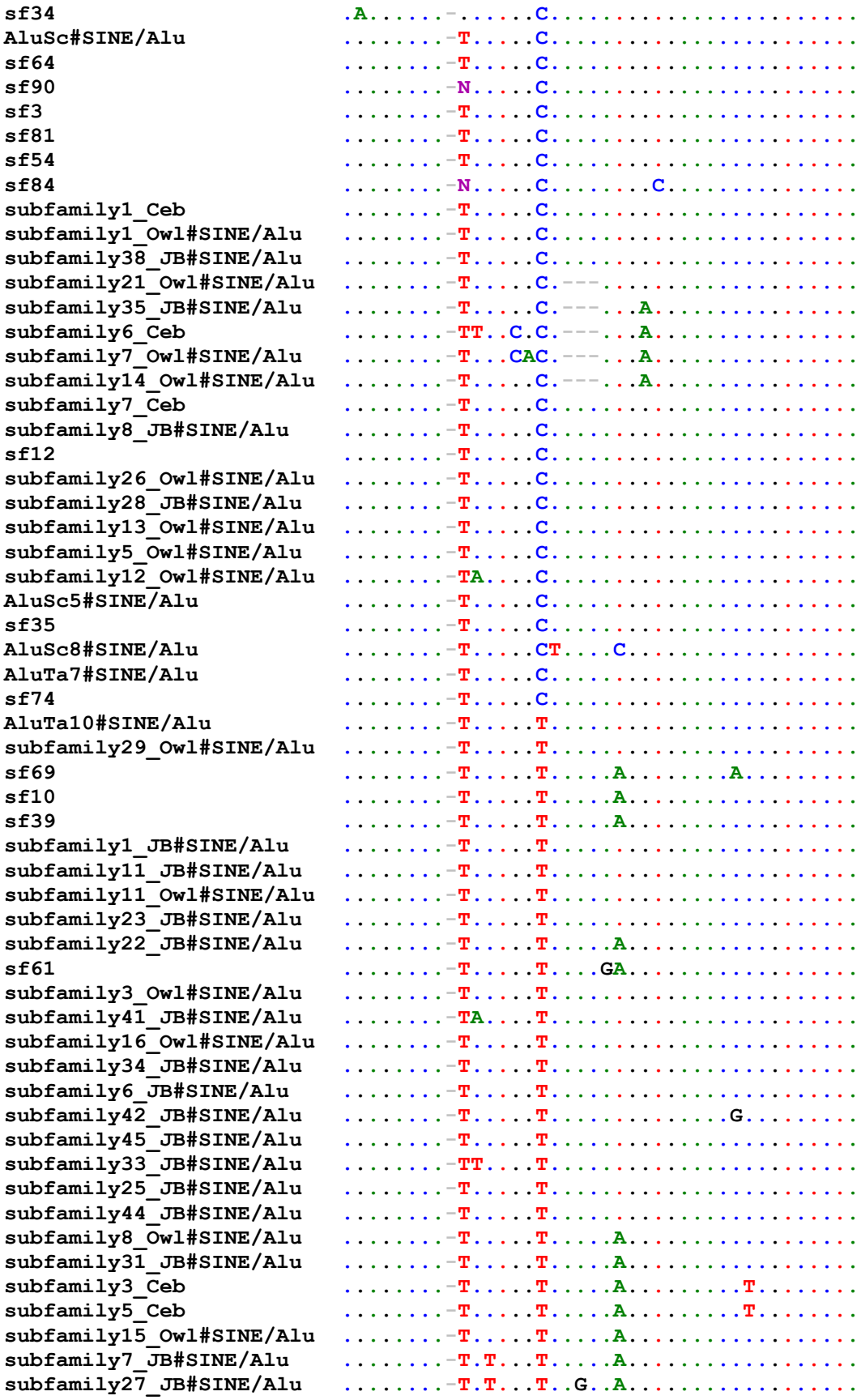
subfamily22_Owl#SINE/Alu
sf55


sf34
AluSc#SINE/Alu
sf64
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subfamily1_Owl#SINE/Alu
subfamily38_JB#SINE/Alu
subfamily21_Owl#SINE/Alu
subfamily35_JB#SINE/Alu
subfamily6_Ceb
subfamily7_Owl#SINE/Alu
subfamily14_Owl#SINE/Alu
subfamily7_Ceb
subfamily8_JB#SINE/Alu
sf12
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subfamily5_Owl#SINE/Alu
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sf35
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subfamily22_JB#SINE/Alu
sf61
subfamily3_Owl#SINE/Alu
subfamily41_JB#SINE/Alu
subfamily16_Owl#SINE/Alu
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subfamily6_JB#SINE/Alu
subfamily42_JB#SINE/Alu
subfamily45_JB#SINE/Alu
subfamily33_JB#SINE/Alu
subfamily25_JB#SINE/Alu
subfamily44_JB#SINE/Alu
subfamily8_Owl#SINE/Alu
subfamily31_JB#SINE/Alu
subfamily3_Ceb
subfamily5_Ceb
subfamily15_Owl#SINE/Alu
subfamily7_JB#SINE/Alu
subfamily27_JB#SINE/Alu

```
subfamily21_JB#SINE/Alu   ........-T.....T....................
subfamily9_JB#SINE/Alu    ........-T.....T....................
subfamily26_JB#SINE/Alu   ........-T.....T....................
subfamily40_JB#SINE/Alu   ........-T.....T....................
subfamily17_JB#SINE/Alu   ........-T.....T.....A..............
AluTa15#SINE/Alu          ........-T.....T....................
sf44                      ........-T.....T....................
subfamily0_JB#SINE/Alu    ........-T.....T....................
sf85                      ........-T.....T....................
sf86                      ........-T.....T....................
sf47                      ........-T.....T....................
sf63                      ........-T.....T....................
sf73                      ........-T.....T....................
sf76                      ........-T.....T....................
subfamily18_JB#SINE/Alu   ........-T.....T....................
subfamily24_JB#SINE/Alu   ........-T.....T....................
subfamily20_Owl#SINE/Alu  ........-T.....T....................
sf37                      ........-T.....T....................
sf38                      ........-T.....T.....A..............
sf42                      ........-T.....T....................
sf46                      ........-T.....T....................
sf52                      ........-T.....T....................
sf53                      ........-T.....T....................
sf60                      ........-T.....T....................
sf62                      ........-T.....T....................
sf71                      ........-T.....T..C.................
sf82                      ........-T.....T....................
subfamily18_Owl#SINE/Alu  ........-T.....T......T..............
subfamily4_Ceb            ........-T.....T...A................
sf66                      ........-T.....T....T...............
sf36                      ........-T..A..T....................
subfamily10_JB#SINE/Alu   ........-T....AT....................
subfamily29_JB#SINE/Alu   ........-T....AT....................
subfamily12_JB#SINE/Alu   ........-T.....T....................
subfamily19_JB#SINE/Alu   ........-T.....T....................
subfamily10_Owl#SINE/Alu  ........-T.....T....................
subfamily17_Owl#SINE/Alu  ........-T.....T......T..............
subfamily23_Owl#SINE/Alu  ........-T.....T....................
sf11                      ........-T..A..T....................
sf4                       ........-T.....T....................
sf51                      ........-T.....T...A................
subfamily25_Owl#SINE/Alu  ........-T.....TA...................
subfamily5_JB#SINE/Alu    ........-A.....T....................
subfamily24_Owl#SINE/Alu  ........-T.....T....................
subfamily37_JB#SINE/Alu   ........-A.....T....................
subfamily39_JB#SINE/Alu   ........-A.....T....................
subfamily19_Owl#SINE/Alu  ........-T.....T......T..............
subfamily2_Ceb            ........-T.....T....................
subfamily8_Ceb            ........-T.....T....................
subfamily14_JB#SINE/Alu   .T......-T.....T....................
subfamily4_JB#SINE/Alu    ........-T.....T....................
subfamily9_Owl#SINE/Alu   ........-T.....T......T..............
sf65                      ........-T.....T....................
subfamily16_JB#SINE/Alu   ........-T.....T....................
subfamily2_JB#SINE/Alu    ........-T.....T.....A..............
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subfamily30_JB#SINE/Alu   ........-T.....T.....A..............
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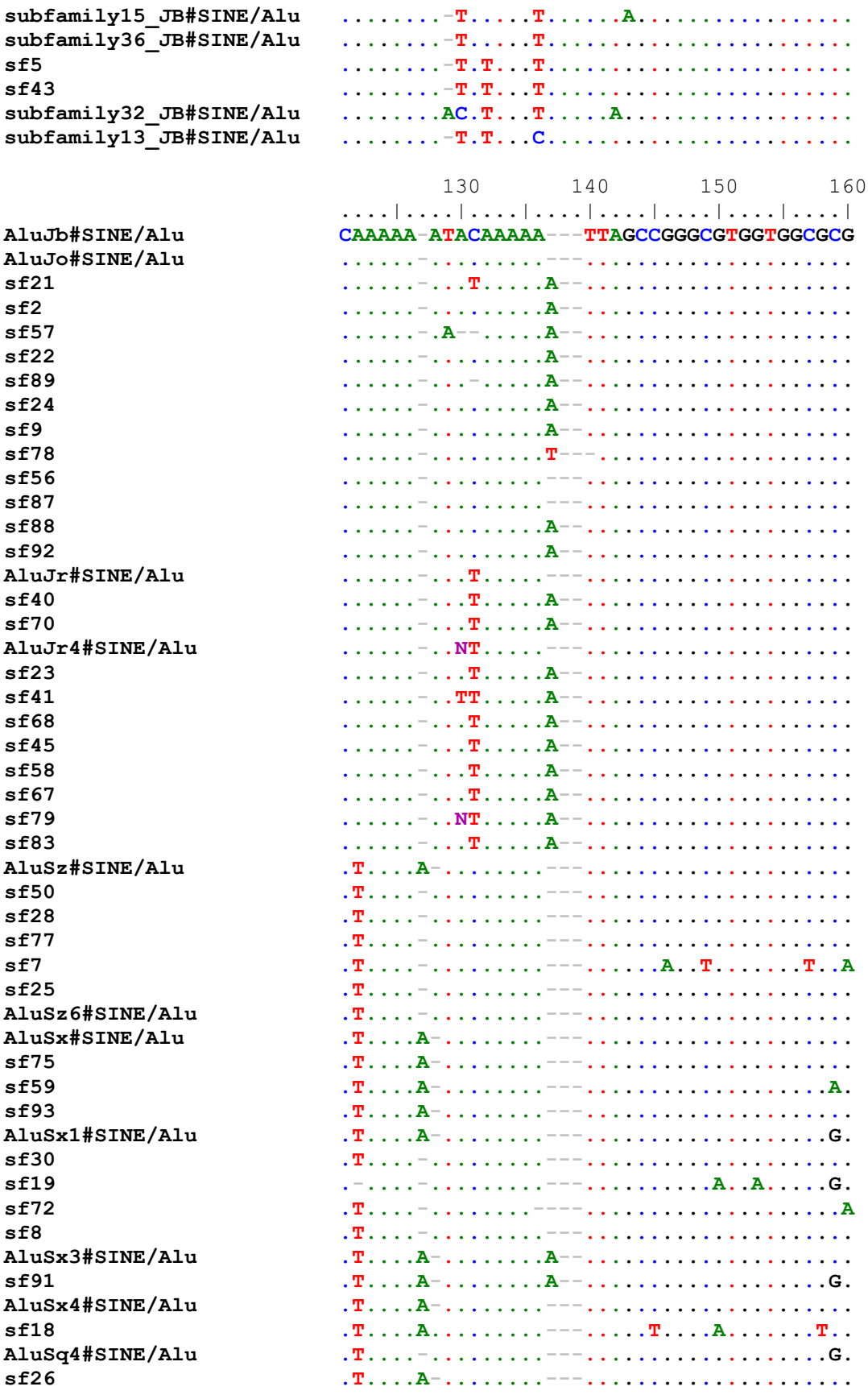
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subfamily36_JB#SINE/Alu
sf5
sf43
subfamily32_JB#SINE/Alu
subfamily13_JB#SINE/Alu
130
140
150
160
AluJb#SINE/Alu
AluJo#SINE/Alu
sf21
sf2
sf57
sf22
sf89
sf24
sf9
sf78
sf56
sf87
sf88
sf92
AluJr#SINE/Alu
sf40
sf70
AluJr4#SINE/Alu
sf23
sf41
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AluSz#SINE/Alu
sf50
sf28
sf77
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AluSz6#SINE/Alu
AluSx#SINE/Alu
sf75
sf59
sf93
AluSx1#SINE/Alu
sf30
sf19
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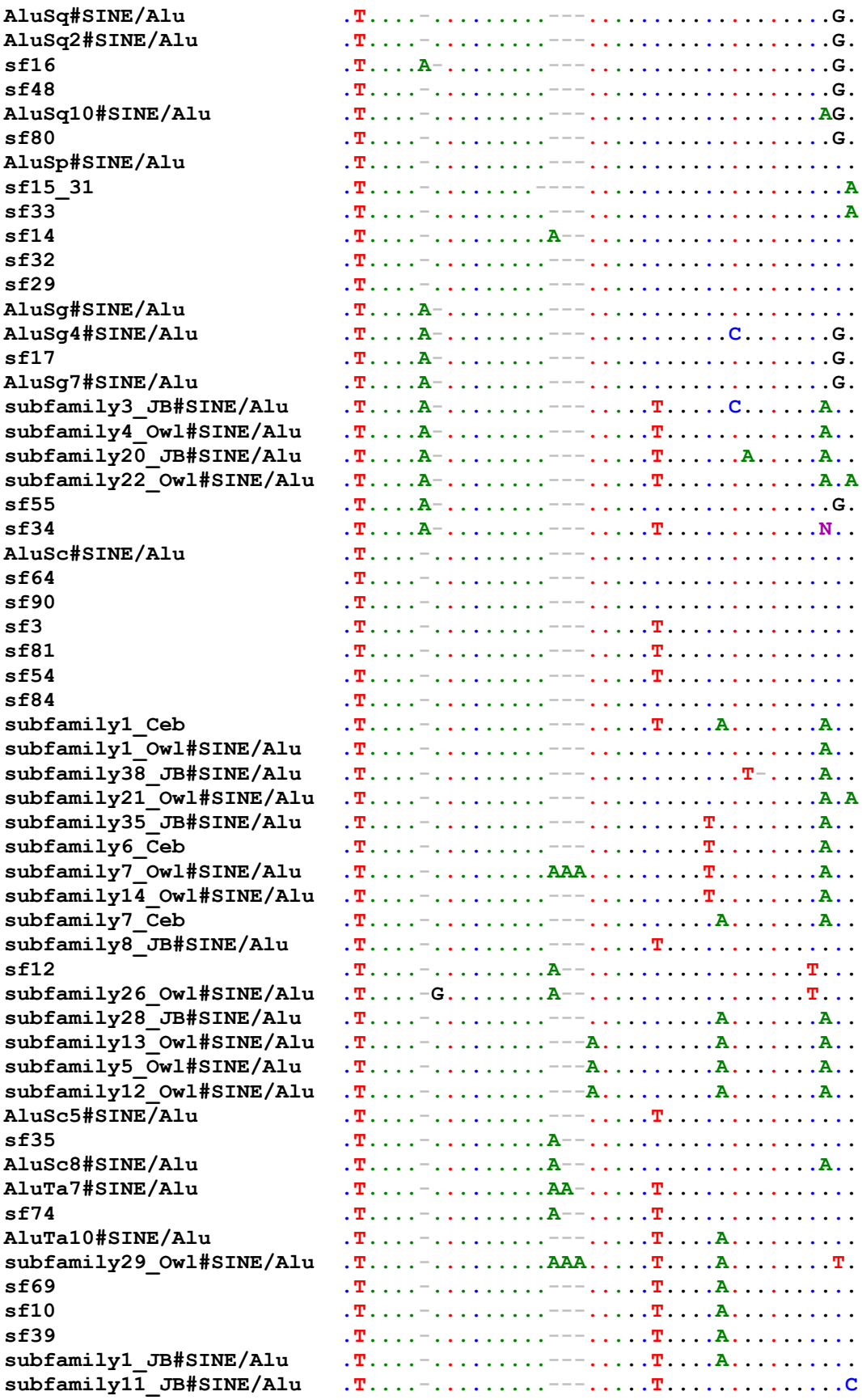
AluSx3#SINE/Alu
sf91
AluSx4#SINE/Alu
sf18
AluSq4#SINE/Alu
sf26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AluSq2#SINE/Alu
sf16
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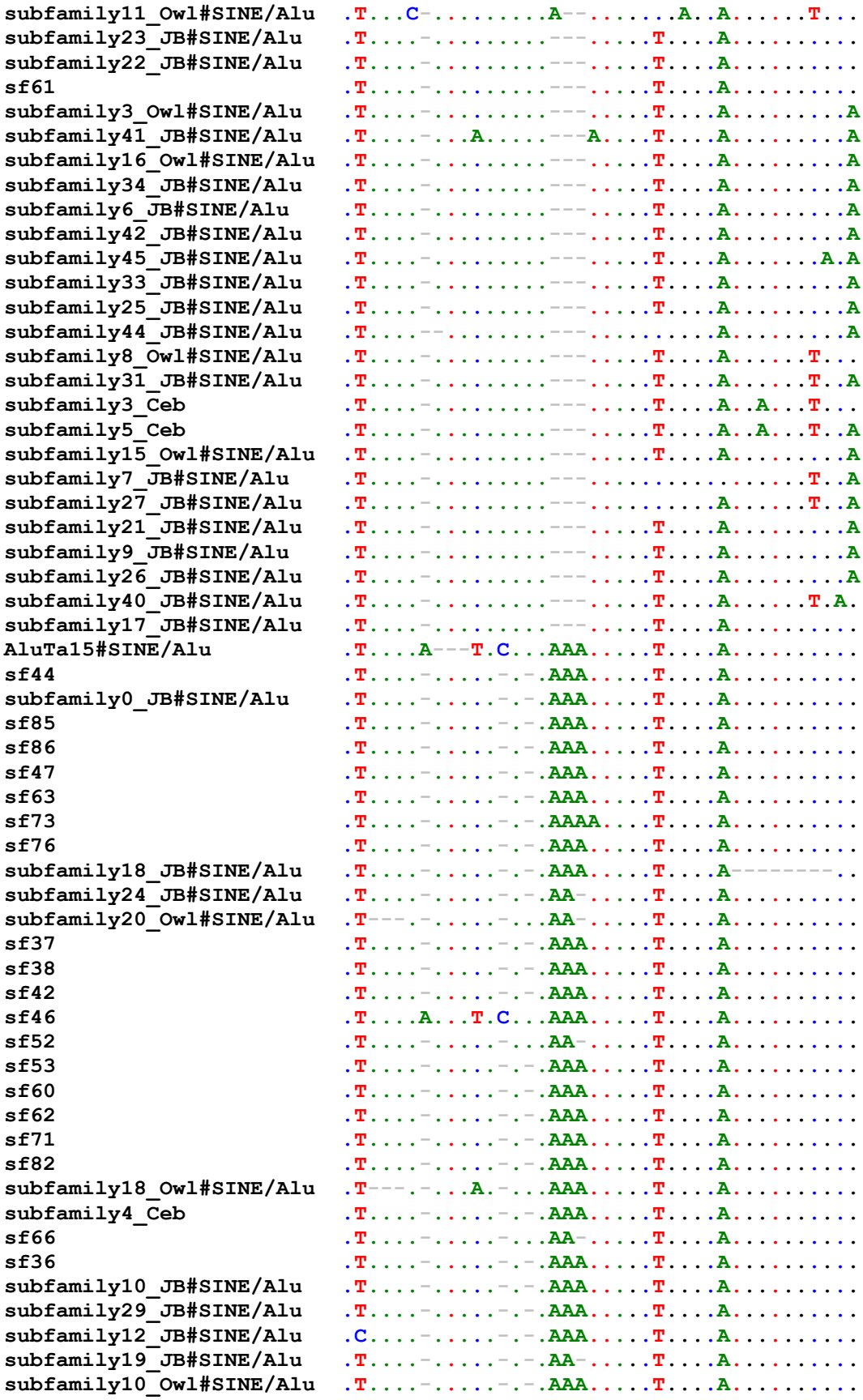
sf80
AluSp#SINE/Alu
sf15_31
sf33
sf14
sf32
sf29
AluSg#SINE/Alu
AluSg4#SINE/Alu
sf17
AluSg7#SINE/Alu
subfamily3_JB#SINE/Alu
subfamily4_Owl#SINE/Alu
subfamily20_JB#SINE/Alu
subfamily22_Owl#SINE/Alu
sf55
sf34
AluSc#SINE/Alu
sf64
sf90
sf3
sf81
sf54
sf84
subfamily1_Ceb
subfamily1_Owl#SINE/Alu
subfamily38_JB#SINE/Alu
subfamily21_Owl#SINE/Alu
subfamily35_JB#SINE/Alu
subfamily6_Ceb
subfamily7_Owl#SINE/Alu
subfamily14_Owl#SINE/Alu
subfamily7_Ceb
subfamily8_JB#SINE/Alu
sf12
subfamily26_Owl#SINE/Alu
subfamily28_JB#SINE/Alu
subfamily13_Owl#SINE/Alu
subfamily5_Owl#SINE/Alu
subfamily12_Owl#SINE/Alu
AluSc5#SINE/Alu
sf35
AluSc8#SINE/Alu
AluTa7#SINE/Alu
sf74
AluTa10#SINE/Alu
subfamily29_Owl#SINE/Alu
sf69
sf10
sf39
subfamily1_JB#SINE/Alu
subfamily11_JB#SINE/Alu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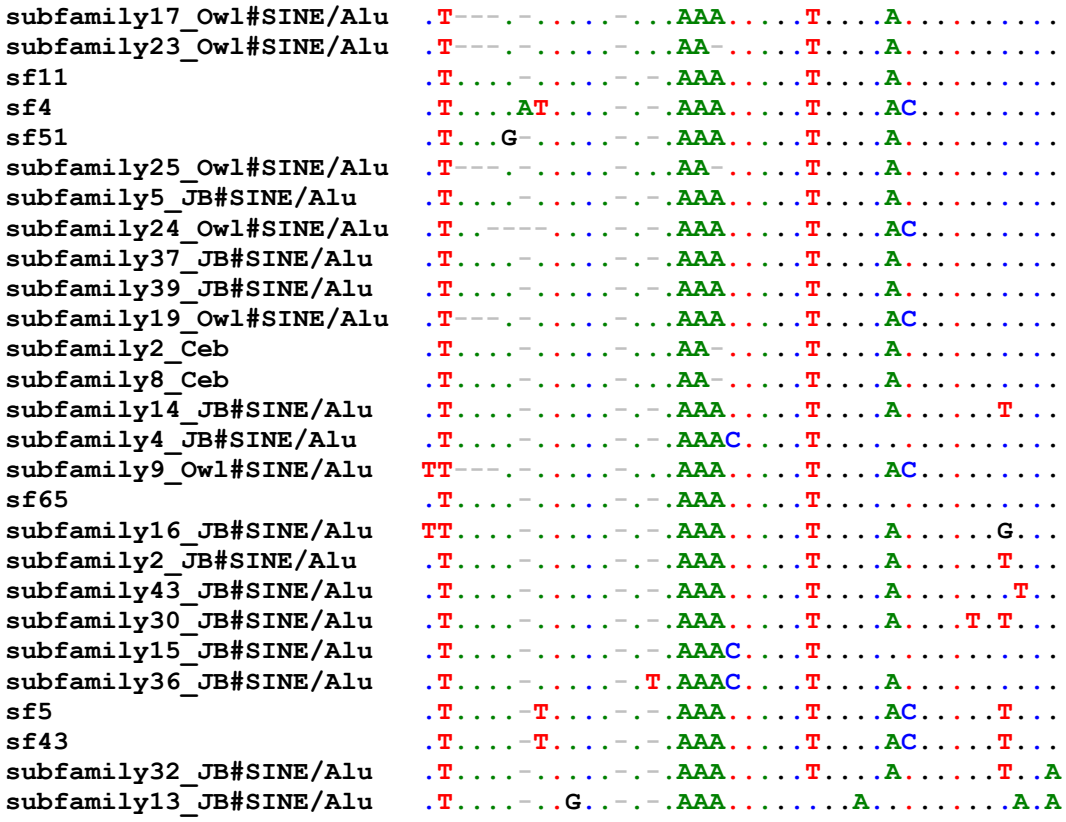
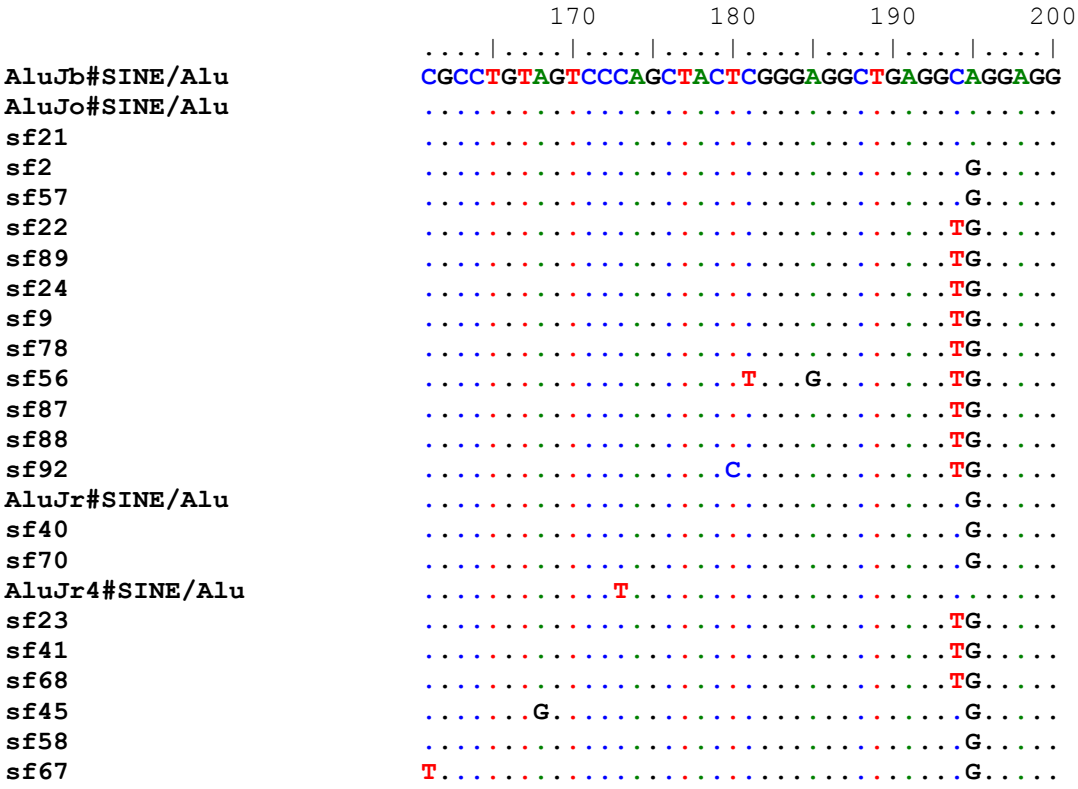
subfamily23_JB#SINE/Alu
subfamily22_JB#SINE/Alu
sf61
subfamily3_Owl#SINE/Alu
subfamily41_JB#SINE/Alu
subfamily16_Owl#SINE/Alu
subfamily34_JB#SINE/Alu
subfamily6_JB#SINE/Alu
subfamily42_JB#SINE/Alu
subfamily45_JB#SINE/Alu
subfamily33_JB#SINE/Alu
subfamily25_JB#SINE/Alu
subfamily44_JB#SINE/Alu
subfamily8_Owl#SINE/Alu
subfamily31_JB#SINE/Alu
subfamily3_Ceb
subfamily5_Ceb
subfamily15_Owl#SINE/Alu
subfamily7_JB#SINE/Alu
subfamily27_JB#SINE/Alu
subfamily21_JB#SINE/Alu
subfamily9_JB#SINE/Alu
subfamily26_JB#SINE/Alu
subfamily40_JB#SINE/Alu
subfamily17_JB#SINE/Alu
AluTa15#SINE/Alu
sf44
subfamily0_JB#SINE/Alu
sf85
sf86
sf47
sf63
sf73
sf76
subfamily18_JB#SINE/Alu
subfamily24_JB#SINE/Alu
subfamily20_Owl#SINE/Alu
sf37
sf38
sf42
sf46
sf52
sf53
sf60
sf62
sf71
sf82
subfamily18_Owl#SINE/Alu
subfamily4_Ceb
sf66
sf36
subfamily10_JB#SINE/Alu
subfamily29_JB#SINE/Alu
subfamily12_JB#SINE/Alu
subfamily19_JB#SINE/Alu
subfamily10_Owl#SINE/Alu


subfamily17_Owl#SINE/Alu
subfamily23_Owl#SINE/Alu
sf11
sf4
sf51
subfamily25_Owl#SINE/Alu
subfamily5_JB#SINE/Alu
subfamily24_Owl#SINE/Alu
subfamily37_JB#SINE/Alu
subfamily39_JB#SINE/Alu
subfamily19_Owl#SINE/Alu
subfamily2_Ceb
subfamily8_Ceb
subfamily14_JB#SINE/Alu
subfamily4_JB#SINE/Alu
subfamily9_Owl#SINE/Alu
sf65
subfamily16_JB#SINE/Alu
subfamily2_JB#SINE/Alu
subfamily43_JB#SINE/Alu
subfamily30_JB#SINE/Alu
subfamily15_JB#SINE/Alu
subfamily36_JB#SINE/Alu
sf5
sf43
subfamily32_JB#SINE/Alu
subfamily13_JB#SINE/Alu


170
180
190
200
AluJb#SINE/Alu
AluJo#SINE/Alu
sf21
sf2
sf57
sf22
sf89
sf24
sf9
sf78
sf56
sf87
sf88
sf92
AluJr#SINE/Alu
sf40
sf70
AluJr4#SINE/Alu
sf23
sf41
sf68
sf45
sf58
sf67

```
sf79                          .............................G.....
sf83                          T............................G.....
AluSz#SINE/Alu                .......A.....................A
sf50                          .......A.....................T...A
sf28                          .......A.....................C...A
sf77                          .......C.....................A
sf7                           .......A.....................CA..A
sf25                          .......A.....................A
AluSz6#SINE/Alu               .......A.....................C...A
AluSx#SINE/Alu                .......A.....................A
sf75                          .......T.....................A
sf59                          .......A.....................A
sf93                          .......A.....................A
AluSx1#SINE/Alu               .......A.....................A
sf30                          .......A.....................A
sf19                          T......A.....................G....A
sf72                          T......A.....................A
sf8                           .......A.....................A
AluSx3#SINE/Alu               .............................A
sf91                          .......A.....................A
AluSx4#SINE/Alu               ............................A..A
sf18                          T......A.....T.....T.....A
AluSq4#SINE/Alu               .......A.....................A
sf26                          .............................A
AluSq#SINE/Alu                .......A.....................A
AluSq2#SINE/Alu               .......A.....................A
sf16                          .......A.....................A
sf48                          .......A.....................A
AluSq10#SINE/Alu              .......A............G...C.....A
sf80                          .......A.....................A
AluSp#SINE/Alu                .......A.....................A
sf15_31                       T......A.....................A
sf33                          T......A.....................A
sf14                          .......A.....................A
sf32                          .......A.....................A
sf29                          .......A.....................A
AluSg#SINE/Alu                .......A.....................A
AluSg4#SINE/Alu               .......A.....................A
sf17                          .......A.....................-..A
AluSg7#SINE/Alu               .......A.....................-..A
subfamily3_JB#SINE/Alu        .......A.....A...............A
subfamily4_Owl#SINE/Alu       .A.....A.....A...............A
subfamily20_JB#SINE/Alu       .A.....A.....A...............A
subfamily22_Owl#SINE/Alu      .......A.....A...............A
sf55                          .......A.....................-..A
sf34                          T......A.....................A
AluSc#SINE/Alu                .............................A
sf64                          .............................A
sf90                          .............................A
sf3                           .............................A
sf81                          .............................A
sf54                          .............................A
sf84                          .............................G....A
subfamily1_Ceb                .............................A
subfamily1_Owl#SINE/Alu       ......G.....................A..A
subfamily38_JB#SINE/Alu       ...........................G.A..A
subfamily21_Owl#SINE/Alu      ......G.....................A..A
```

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subfamily35_JB#SINE/Alu   ..............................G.A..A
subfamily6_Ceb            ..............................G.A..A
subfamily7_Owl#SINE/Alu   ..............................G.A..A
subfamily14_Owl#SINE/Alu  ..............................G.A..A
subfamily7_Ceb            .......G.......................G.A..A
subfamily8_JB#SINE/Alu    T.....................................A
sf12                      T.....................................A
subfamily26_Owl#SINE/Alu  T.....................................A
subfamily28_JB#SINE/Alu   T......G.....................G.A..A
subfamily13_Owl#SINE/Alu  T......G.....................G.A..A
subfamily5_Owl#SINE/Alu   T......G.....................G.A..A
subfamily12_Owl#SINE/Alu  T......G.....................TG.A..A
AluSc5#SINE/Alu           T.......A.....................A
sf35                      ..............................A
AluSc8#SINE/Alu           ..............................A
AluTa7#SINE/Alu           ..............................A
sf74                      ..............................A
AluTa10#SINE/Alu          ..............................A
subfamily29_Owl#SINE/Alu  ..............................A
sf69                      ..............................A
sf10                      ..............................A
sf39                      ..............................A
subfamily1_JB#SINE/Alu    T.....................................A
subfamily11_JB#SINE/Alu   T.......A........---.....................A
subfamily11_Owl#SINE/Alu  T.....................................A
subfamily23_JB#SINE/Alu   T.....................................A
subfamily22_JB#SINE/Alu   T.....................................A
sf61                      T.......A.................G...........A
subfamily3_Owl#SINE/Alu   ..............................A
subfamily41_JB#SINE/Alu   ..............................A
subfamily16_Owl#SINE/Alu  ..............................A
subfamily34_JB#SINE/Alu   ................T.....................A
subfamily6_JB#SINE/Alu    ..............................A
subfamily42_JB#SINE/Alu   ..............................A
subfamily45_JB#SINE/Alu   ..................C...................A
subfamily33_JB#SINE/Alu   ..............................A
subfamily25_JB#SINE/Alu   ..............................A
subfamily44_JB#SINE/Alu   ..................A...................A
subfamily8_Owl#SINE/Alu   ..............................A
subfamily31_JB#SINE/Alu   T.....................................A
subfamily3_Ceb            T.....................................A
subfamily5_Ceb            T.............................C....A
subfamily15_Owl#SINE/Alu  ..............................A
subfamily7_JB#SINE/Alu    ..............................A
subfamily27_JB#SINE/Alu   ..............................A
subfamily21_JB#SINE/Alu   ..................A...................A
subfamily9_JB#SINE/Alu    ..................A...................A
subfamily26_JB#SINE/Alu   ..................A...................A
subfamily40_JB#SINE/Alu   T.....................................A
subfamily17_JB#SINE/Alu   ...........T.....................T.....A
AluTa15#SINE/Alu          T.......A...........A...................A
sf44                      T.......A...........A...................A
subfamily0_JB#SINE/Alu    T.......A...........A...................A
sf85                      T.......A...........A...................A
sf86                      T.......A...........A...................A
sf47                      T.......A...........A...................A
sf63                      T.......A...........A...................A
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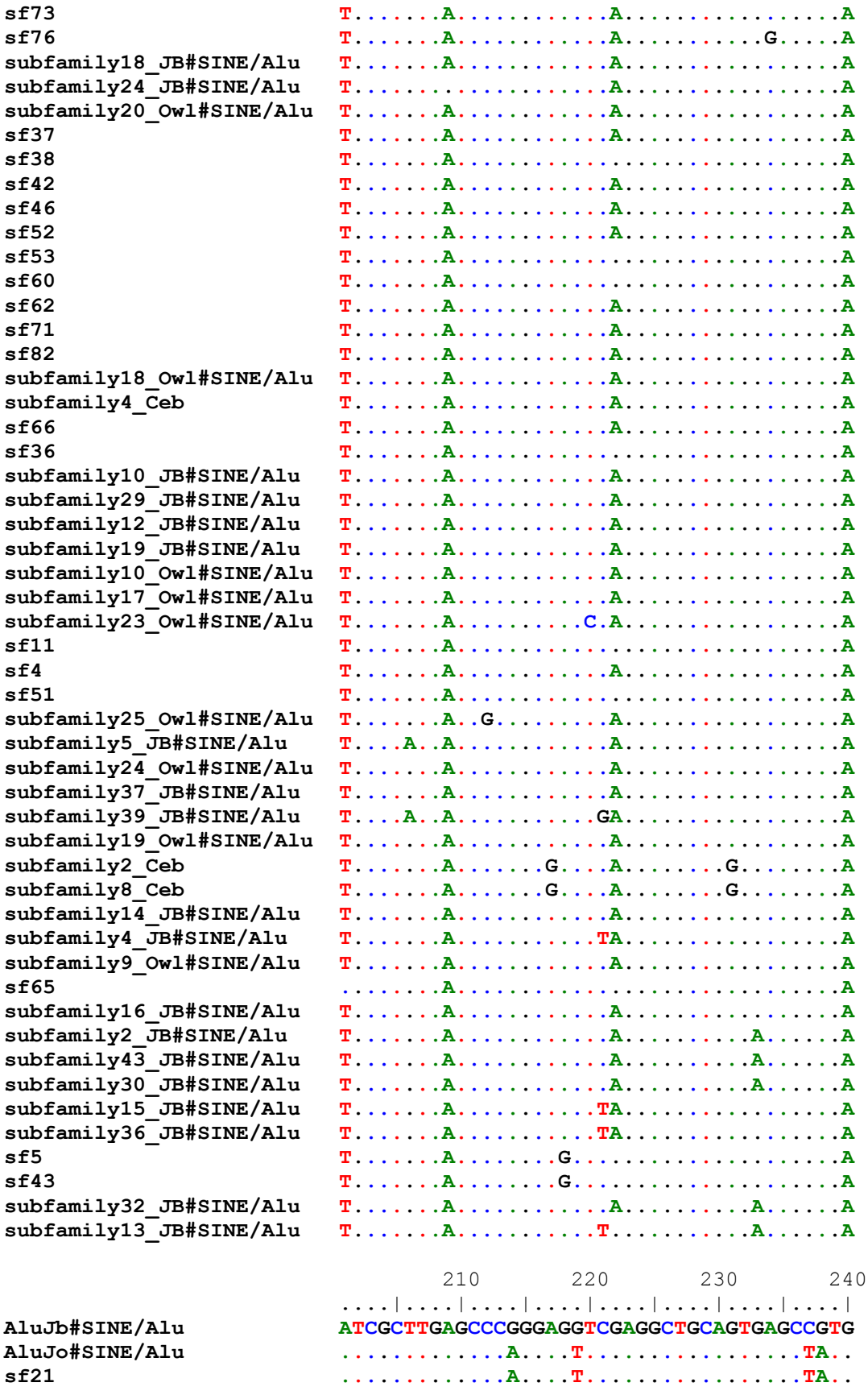
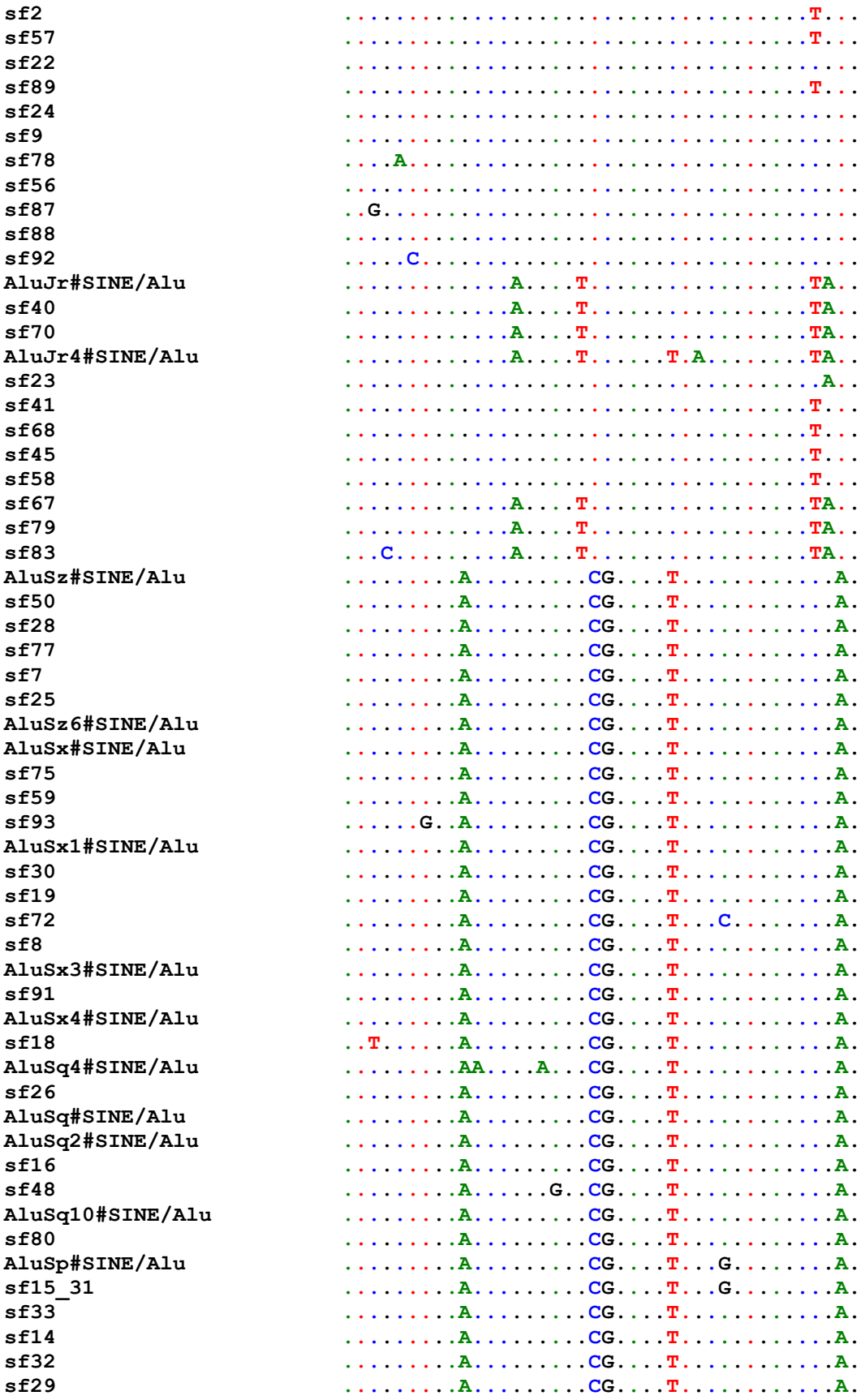

sf73
sf76
subfamily18_JB#SINE/Alu
subfamily24_JB#SINE/Alu
subfamily20_Owl#SINE/Alu
sf37
sf38
sf42
sf46
sf52
sf53
sf60
sf62
sf71
sf82
subfamily18_Owl#SINE/Alu
subfamily4_Ceb
sf66
sf36
subfamily10_JB#SINE/Alu
subfamily29_JB#SINE/Alu
subfamily12_JB#SINE/Alu
subfamily19_JB#SINE/Alu
subfamily10_Owl#SINE/Alu
subfamily17_Owl#SINE/Alu
subfamily23_Owl#SINE/Alu
sf11
sf4
sf51
subfamily25_Owl#SINE/Alu
subfamily5_JB#SINE/Alu
subfamily24_Owl#SINE/Alu
subfamily37_JB#SINE/Alu
subfamily39_JB#SINE/Alu
subfamily19_Owl#SINE/Alu
subfamily2_Ceb
subfamily8_Ceb
subfamily14_JB#SINE/Alu
subfamily4_JB#SINE/Alu
subfamily9_Owl#SINE/Alu
sf65
subfamily16_JB#SINE/Alu
subfamily2_JB#SINE/Alu
subfamily43_JB#SINE/Alu
subfamily30_JB#SINE/Alu
subfamily15_JB#SINE/Alu
subfamily36_JB#SINE/Alu
sf5
sf43
subfamily32_JB#SINE/Alu
subfamily13_JB#SINE/Alu
210
220
230
240
AluJb#SINE/Alu
ATCGCTTGAGCCCGGGAGGTCGAGGCTGCAGTGAGCCGTG
AluJo#SINE/Alu
sf21


sf2
sf57
sf22
sf89
sf24
sf9
sf78
sf56
sf87
sf88
sf92
AluJr#SINE/Alu
sf40
sf70
AluJr4#SINE/Alu
sf23
sf41
sf68
sf45
sf58
sf67
sf79
sf83
AluSz#SINE/Alu
sf50
sf28
sf77
sf7
sf25
AluSz6#SINE/Alu
AluSx#SINE/Alu
sf75
sf59
sf93
AluSx1#SINE/Alu
sf30
sf19
sf72
sf8
AluSx3#SINE/Alu
sf91
AluSx4#SINE/Alu
sf18
AluSq4#SINE/Alu
sf26
AluSq#SINE/Alu
AluSq2#SINE/Alu
sf16
sf48
AluSq10#SINE/Alu
sf80
AluSp#SINE/Alu
sf15_31
sf33
sf14
sf32
sf29

```
AluSg#SINE/Alu                .........A.........CG....T...........A.
AluSg4#SINE/Alu               .........A.........CG....T...........A.
sf17                          .........A.........CG....T...........A.
AluSg7#SINE/Alu               ..T......A.........CG....T...........A.
subfamily3_JB#SINE/Alu        .........A..T......CG....T...........A.
subfamily4_Owl#SINE/Alu       .........A..T......CG....T...........A.
subfamily20_JB#SINE/Alu       .........A..T......CG....T...........A.
subfamily22_Owl#SINE/Alu      ..T..C...A..T......CA....T...........AA.
sf55                          .CT......A.........CG....T...........A.
sf34                          ..T......A.........CG....T...........A.
AluSc#SINE/Alu                .........A.........CG....T...........A.
sf64                          ..A......A.........CG....T...........A.
sf90                          .........A.........CG....T...........A.
sf3                           .........A.........CG....T...........A.
sf81                          .........A.........CG....T...........A.
sf54                          .........A.........CG....T...........A.
sf84                          .........A.........CG....T...........A.
subfamily1_Ceb                ..T......A...A.....CG....T...........A.
subfamily1_Owl#SINE/Alu       .........A...A.....CG....T...........A.
subfamily38_JB#SINE/Alu       .........A...A.....CG....T...........A.
subfamily21_Owl#SINE/Alu      .........A...A......G....T...........A.
subfamily35_JB#SINE/Alu       .........A...A.....CG....T...........A.
subfamily6_Ceb                .........A...A.....CG....T...........A.
subfamily7_Owl#SINE/Alu       .........A...A.....CG....T...........A.
subfamily14_Owl#SINE/Alu      .........A...A.....CG....T...........A.
subfamily7_Ceb                .........A...A.....CG....T...........A.
subfamily8_JB#SINE/Alu        ..T......A...A.....CG....T...........A.
sf12                          ..T......AA....A.AACG..A.T...........G.
subfamily26_Owl#SINE/Alu      ..T......AA..A.A.AACG..A.T...........G.
subfamily28_JB#SINE/Alu       .........A...A.....CG....T...........A.
subfamily13_Owl#SINE/Alu      .........A...A.....CG....T...........A.
subfamily5_Owl#SINE/Alu       .........AT..A.....CG....T...........A.
subfamily12_Owl#SINE/Alu      .........AT..A.....CG....T...........A.
AluSc5#SINE/Alu               .........A..A.....TCG....T...........A.
sf35                          .........A.........CG....T...........A.
AluSc8#SINE/Alu               .........A.........CG....T...........A.
AluTa7#SINE/Alu               ..T......A.........CG....T...........A.
sf74                          .........A.........CG....T...........A.
AluTa10#SINE/Alu              ..T......A...A.....CG....T...G........A.
subfamily29_Owl#SINE/Alu      ..T......A...A.....CG....T...G........A.
sf69                          ..T......A...A.....CG....T...G........A.
sf10                          ..T......A...A.....CG....T...G........A.
sf39                          ..T..C...A...A.....CG....T...G........A.
subfamily1_JB#SINE/Alu        ..T......A...A.....CG....T...G........A.
subfamily11_JB#SINE/Alu       ..T......A...A.....CG....T...G........A.
subfamily11_Owl#SINE/Alu      ..T......A...A.....CG....T...G........A.
subfamily23_JB#SINE/Alu       ..T......A...A.....CG....T...G........A.
subfamily22_JB#SINE/Alu       ..T......A...A.....CG....T...G........A.
sf61                          ..T......A...A.A...CG....T...G........A.
subfamily3_Owl#SINE/Alu       ..T......A...A.....CG....T...G........A.
subfamily41_JB#SINE/Alu       ..T......A...A....ACG....T...G........A.
subfamily16_Owl#SINE/Alu      ..T......A...A.....CG....T...G........A.
subfamily34_JB#SINE/Alu       ..T......A...A.....CG....T...G........A.
subfamily6_JB#SINE/Alu        ..T......A...A....ACG....T...G........A.
subfamily42_JB#SINE/Alu       ..T......A...A....ACG....T...G........A.
subfamily45_JB#SINE/Alu       ..T......A...A....ACG....T...G........A.
subfamily33_JB#SINE/Alu       ..T......A...A.....CG....T...G........A.
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subfamily25_JB#SINE/Alu   ..T.....A...A....ACG....T...G........A.
subfamily44_JB#SINE/Alu   ..T.....A........CCG..A.T..........A.A.
subfamily8_Owl#SINE/Alu   ..T.....A...A.....CG....T...G........A.
subfamily31_JB#SINE/Alu   ..T.....A...A.....CG....T...G........A.
subfamily3_Ceb            ..T.....A...A.....CG....T...G........A.
subfamily5_Ceb            ..T.....A...A.....CG....T...G........A.
subfamily15_Owl#SINE/Alu  ..T.....A...A.....CG....T...G........A.
subfamily7_JB#SINE/Alu    ..T.....A...A.....CG....T...G........A.
subfamily27_JB#SINE/Alu   ..T.....A...A.....CG....T...G........A.
subfamily21_JB#SINE/Alu   ..T.....A...A.....CG....T...G........A.
subfamily9_JB#SINE/Alu    ..T.....A...A.....CG....T...G........A.
subfamily26_JB#SINE/Alu   ..T.....A...A..G..CG....T...G........A.
subfamily40_JB#SINE/Alu   ..T.....A...A.....CG....T...G........A.
subfamily17_JB#SINE/Alu   ..T.....A.T.A.....CG....T...G........A.
AluTa15#SINE/Alu          ..T..C...A...A.....CG....T...G........A.
sf44                      ..T..C...A...A.....CG....T...G........A.
subfamily0_JB#SINE/Alu    ..T..C...A...A.....CG....T...G........A.
sf85                      ..T..C...A...A.....CG....T...G........A.
sf86                      ..T..C...A...A.....CG....T...G.....G.A.
sf47                      ..T..C...A...A.....CG....T...G........A.
sf63                      ..T..C...A...A.....CG....T...G........A.
sf73                      ..T..C...A...A.....CG....T...G........A.
sf76                      ..T..C...A...A.....CG....T...G........A.
subfamily18_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily24_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily20_Owl#SINE/Alu  ..T..C...A...A.....CG....T...G........A.
sf37                      ..T..C...A...A.....CG....T...G........A.
sf38                      ..T..C...A...A.....CG....T...G........A.
sf42                      ..T..C...A...A.....CG....T...G........A.
sf46                      ..T..C...A...A.....CG....T...G........A.
sf52                      ..T..C...A...A.....CG....T...G........A.
sf53                      ..T..C...T...A.....CG....T...G........A.
sf60                      ..T..C...A...A.....CG....T...G........A.
sf62                      ..T..C...A...A.....CG....T..AG........A.
sf71                      ..T..C...A...A.....CG....T...G........A.
sf82                      ..T..C...A...A.....CG....T...G........A.
subfamily18_Owl#SINE/Alu  ..T..C...A...A.....CG....T...G........A.
subfamily4_Ceb            ..T..C...A...A.....CG....T...G........A.
sf66                      ..T..C...A...A.....CG....T...G........A.
sf36                      ..T..C...A...A.....CG....T...G........A.
subfamily10_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily29_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily12_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily19_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily10_Owl#SINE/Alu  ..T..C...A...A.....CG....T...GA.......A.
subfamily17_Owl#SINE/Alu  ..T..C...A...A.....CG....T...G........A.
subfamily23_Owl#SINE/Alu  ..T..C...A...A.....CG....T...G........A.
sf11                      ..T..C.......A.....CG....T...G........A.
sf4                       ..T..C...A...A..G..CG....T...G........A.
sf51                      ..T..C...A...A.....CG....T...G........A.
subfamily25_Owl#SINE/Alu  ..T..C...A...A.....CG....T...G........A.
subfamily5_JB#SINE/Alu    ..T..C...A...A.....CG....T...G........A.
subfamily24_Owl#SINE/Alu  ..T..C...A...A.....CG...AT...G........A.
subfamily37_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........AT
subfamily39_JB#SINE/Alu   ..T..C...A...A.....CG....T...G........A.
subfamily19_Owl#SINE/Alu  ..T..C...A...A.....CG....T...G........A.
subfamily2_Ceb            ..T..C...A.........CG....T...G........A.
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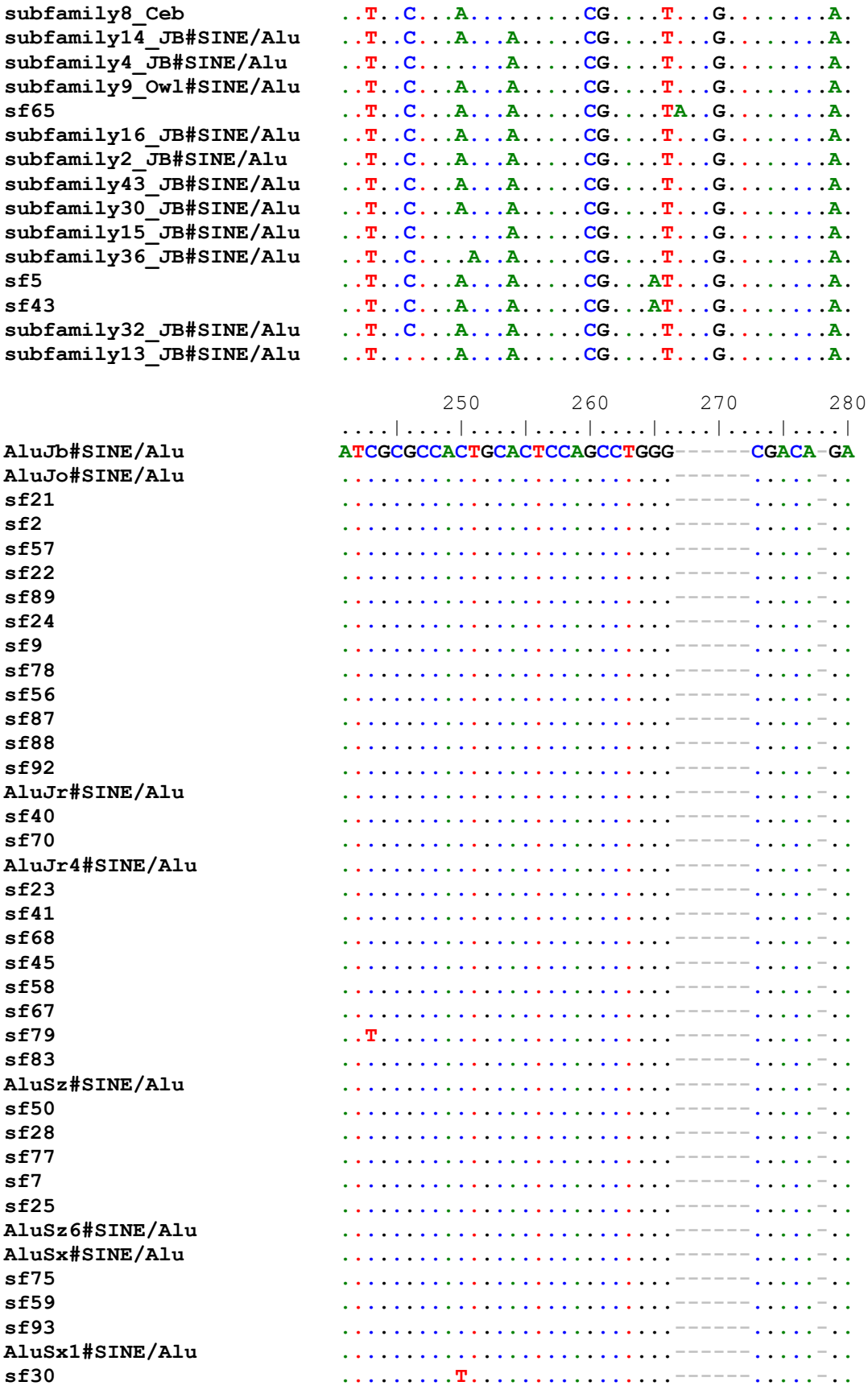
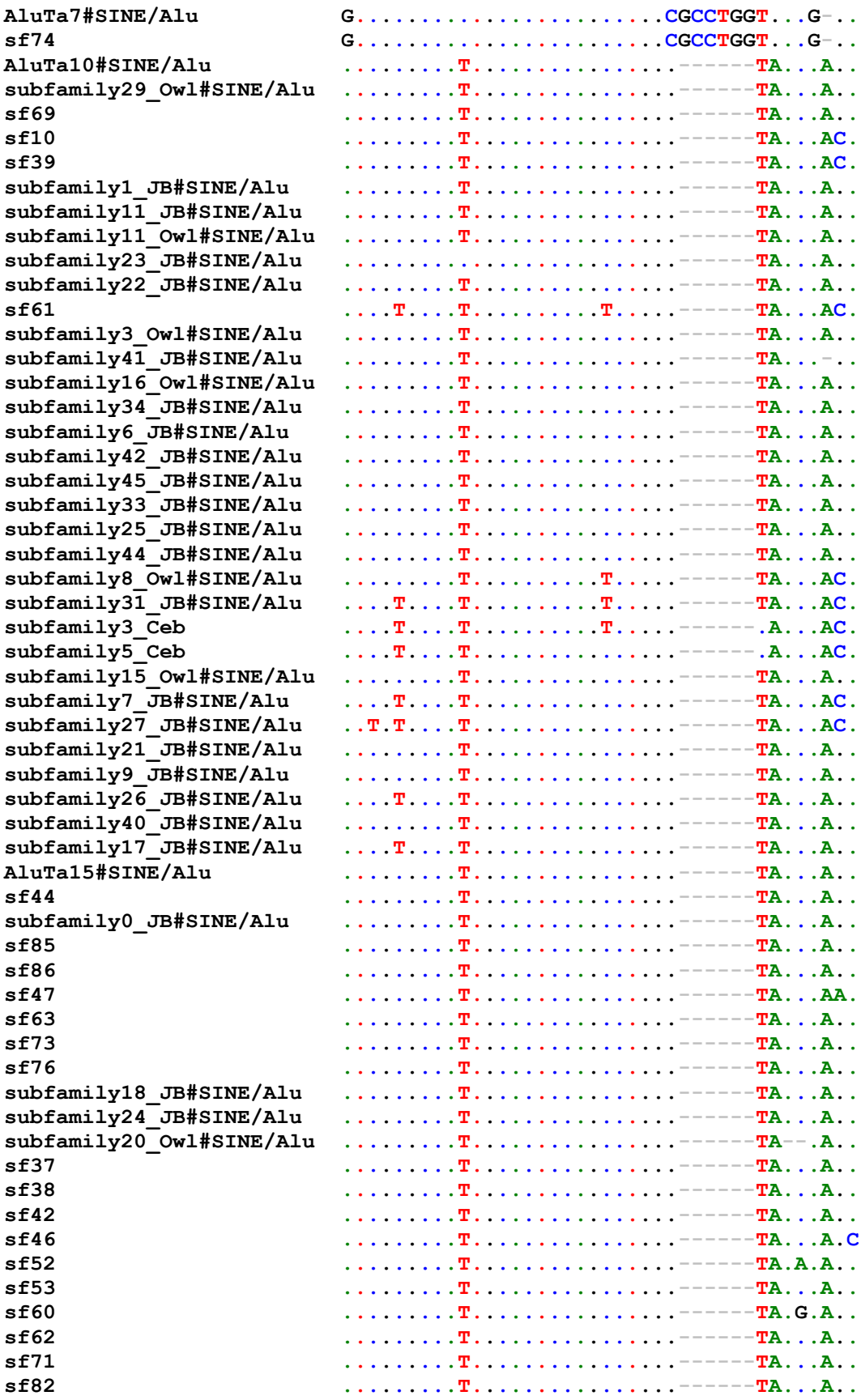
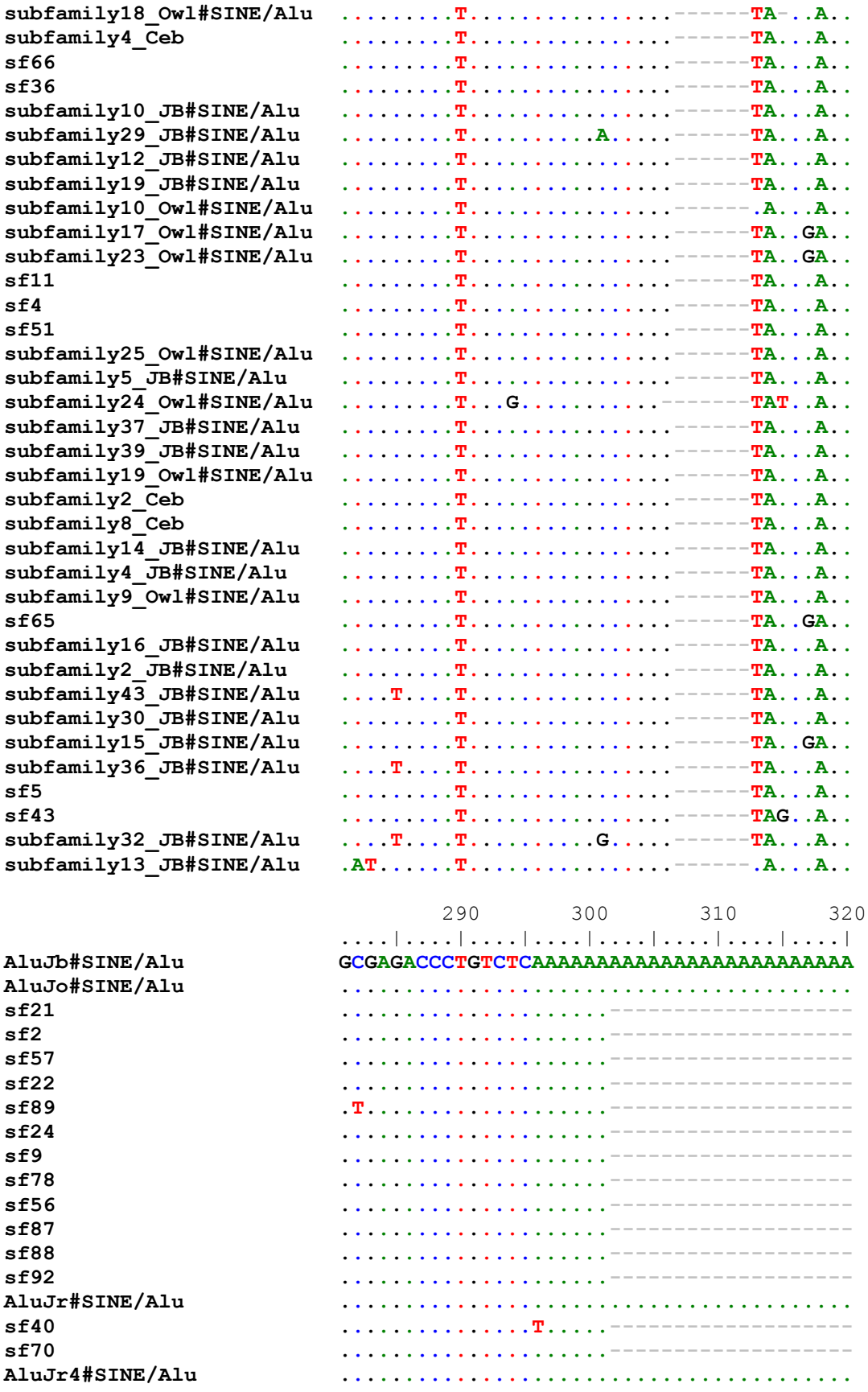

subfamily8_Ceb ..T..C...A.........CG....T...G........A.
subfamily14_JB#SINE/Alu ..T..C...A...A.....CG....T...G........A.
subfamily4_JB#SINE/Alu ..T..C.......A.....CG....T...G........A.
subfamily9_Owl#SINE/Alu ..T..C...A...A.....CG....T...G........A.
sf65 ..T..C...A...A.....CG....TA..G........A.
subfamily16_JB#SINE/Alu ..T..C...A...A.....CG....T...G........A.
subfamily2_JB#SINE/Alu ..T..C...A...A.....CG....T...G........A.
subfamily43_JB#SINE/Alu ..T..C...A...A.....CG....T...G........A.
subfamily30_JB#SINE/Alu ..T..C...A...A.....CG....T...G........A.
subfamily15_JB#SINE/Alu ..T..C.......A.....CG....T...G........A.
subfamily36_JB#SINE/Alu ..T..C....A..A.....CG....T...G........A.
sf5 ..T..C...A...A.....CG...AT...G........A.
sf43 ..T..C...A...A.....CG...AT...G........A.
subfamily32_JB#SINE/Alu ..T..C...A...A.....CG....T...G........A.
subfamily13_JB#SINE/Alu ..T.....A...A.....CG....T...G........A.
250
260
270
280
AluJb#SINE/Alu ATCGCGCCACTGCACTCCAGCCTGGG------CGACA-GA
AluJo#SINE/Alu ..........................------.....-..
sf21 ..........................------.....-..
sf2 ..........................------.....-..
sf57 ..........................------.....-..
sf22 ..........................------.....-..
sf89 ..........................------.....-..
sf24 ..........................------.....-..
sf9 ..........................------.....-..
sf78 ..........................------.....-..
sf56 ..........................------.....-..
sf87 ..........................------.....-..
sf88 ..........................------.....-..
sf92 ..........................------.....-..
AluJr#SINE/Alu ..........................------.....-..
sf40 ..........................------.....-..
sf70 ..........................------.....-..
AluJr4#SINE/Alu ..........................------.....-..
sf23 ..........................------.....-..
sf41 ..........................------.....-..
sf68 ..........................------.....-..
sf45 ..........................------.....-..
sf58 ..........................------.....-..
sf67 ..........................------.....-..
sf79 ..T.......................------.....-..
sf83 ..........................------.....-..
AluSz#SINE/Alu ..........................------.....-..
sf50 ..........................------.....-..
sf28 ..........................------.....-..
sf77 ..........................------.....-..
sf7 ..........................------.....-..
sf25 ..........................------.....-..
AluSz6#SINE/Alu ..........................------.....-..
AluSx#SINE/Alu ..........................------.....-..
sf75 ..........................------.....-..
sf59 ..........................------.....-..
sf93 ..........................------.....-..
AluSx1#SINE/Alu ..........................------.....-..
sf30 .........T..............------.....-..


sf19
sf72
sf8
AluSx3#SINE/Alu
sf91
AluSx4#SINE/Alu
sf18
AluSq4#SINE/Alu
sf26
AluSq#SINE/Alu
AluSq2#SINE/Alu
sf16
sf48
AluSq10#SINE/Alu
sf80
AluSp#SINE/Alu
sf15_31
sf33
sf14
sf32
sf29
AluSg#SINE/Alu
AluSg4#SINE/Alu
sf17
AluSg7#SINE/Alu
subfamily3_JB#SINE/Alu
subfamily4_Owl#SINE/Alu
subfamily20_JB#SINE/Alu
subfamily22_Owl#SINE/Alu
sf55
sf34
AluSc#SINE/Alu
sf64
sf90
sf3
sf81
sf54
sf84
subfamily1_Ceb
subfamily1_Owl#SINE/Alu
subfamily38_JB#SINE/Alu
subfamily21_Owl#SINE/Alu
subfamily35_JB#SINE/Alu
subfamily6_Ceb
subfamily7_Owl#SINE/Alu
subfamily14_Owl#SINE/Alu
subfamily7_Ceb
subfamily8_JB#SINE/Alu
sf12
subfamily26_Owl#SINE/Alu
subfamily28_JB#SINE/Alu
subfamily13_Owl#SINE/Alu
subfamily5_Owl#SINE/Alu
subfamily12_Owl#SINE/Alu
AluSc5#SINE/Alu
sf35
AluSc8#SINE/Alu


AluTa7#SINE/Alu
sf74
AluTa10#SINE/Alu
subfamily29_Owl#SINE/Alu
sf69
sf10
sf39
subfamily1_JB#SINE/Alu
subfamily11_JB#SINE/Alu
subfamily11_Owl#SINE/Alu
subfamily23_JB#SINE/Alu
subfamily22_JB#SINE/Alu
sf61
subfamily3_Owl#SINE/Alu
subfamily41_JB#SINE/Alu
subfamily16_Owl#SINE/Alu
subfamily34_JB#SINE/Alu
subfamily6_JB#SINE/Alu
subfamily42_JB#SINE/Alu
subfamily45_JB#SINE/Alu
subfamily33_JB#SINE/Alu
subfamily25_JB#SINE/Alu
subfamily44_JB#SINE/Alu
subfamily8_Owl#SINE/Alu
subfamily31_JB#SINE/Alu
subfamily3_Ceb
subfamily5_Ceb
subfamily15_Owl#SINE/Alu
subfamily7_JB#SINE/Alu
subfamily27_JB#SINE/Alu
subfamily21_JB#SINE/Alu
subfamily9_JB#SINE/Alu
subfamily26_JB#SINE/Alu
subfamily40_JB#SINE/Alu
subfamily17_JB#SINE/Alu
AluTa15#SINE/Alu
sf44
subfamily0_JB#SINE/Alu
sf85
sf86
sf47
sf63
sf73
sf76
subfamily18_JB#SINE/Alu
subfamily24_JB#SINE/Alu
subfamily20_Owl#SINE/Alu
sf37
sf38
sf42
sf46
sf52
sf53
sf60
sf62
sf71
sf82


subfamily18_Owl#SINE/Alu
subfamily4_Ceb
sf66
sf36
subfamily10_JB#SINE/Alu
subfamily29_JB#SINE/Alu
subfamily12_JB#SINE/Alu
subfamily19_JB#SINE/Alu
subfamily10_Owl#SINE/Alu
subfamily17_Owl#SINE/Alu
subfamily23_Owl#SINE/Alu
sf11
sf4
sf51
subfamily25_Owl#SINE/Alu
subfamily5_JB#SINE/Alu
subfamily24_Owl#SINE/Alu
subfamily37_JB#SINE/Alu
subfamily39_JB#SINE/Alu
subfamily19_Owl#SINE/Alu
subfamily2_Ceb
subfamily8_Ceb
subfamily14_JB#SINE/Alu
subfamily4_JB#SINE/Alu
subfamily9_Owl#SINE/Alu
sf65
subfamily16_JB#SINE/Alu
subfamily2_JB#SINE/Alu
subfamily43_JB#SINE/Alu
subfamily30_JB#SINE/Alu
subfamily15_JB#SINE/Alu
subfamily36_JB#SINE/Alu
sf5
sf43
subfamily32_JB#SINE/Alu
subfamily13_JB#SINE/Alu
290
300
310
320
AluJb#SINE/Alu
AluJo#SINE/Alu
sf21
sf2
sf57
sf22
sf89
sf24
sf9
sf78
sf56
sf87
sf88
sf92
AluJr#SINE/Alu
sf40
sf70
AluJr4#SINE/Alu

```
sf23                          ....................----------
sf41                          ....................----------
sf68                          ....................----------
sf45                          ....................----------
sf58                          ....................----------
sf67                          ....................----------
sf79                          ....................----------
sf83                          ....................----------
AluSz#SINE/Alu                .......T.C.............................
sf50                          .......T.............----------
sf28                          .......T.............----------
sf77                          .......T.C...........----------
sf7                           .......T.C...........----------
sf25                          .......T.............----------
AluSz6#SINE/Alu               .......T.....................................
AluSx#SINE/Alu                .......T.C...........................
sf75                          .......T.C...........----------
sf59                          .......T.C...........----------
sf93                          .......T.C...........----------
AluSx1#SINE/Alu               .......T.C...........................
sf30                          .......T.C...........----------
sf19                          .......T.C...........----------
sf72                          ....A..T.C...........----------
sf8                           ....A..T.C...........----------
AluSx3#SINE/Alu               .......T.C...........................
sf91                          .......T.C...........----------
AluSx4#SINE/Alu               .......T.C...........................
sf18                          .......T.CA..........----------
AluSq4#SINE/Alu               ....A..T.C...........................
sf26                          .......T.C...........----------
AluSq#SINE/Alu                ....A..T.C...........................
AluSq2#SINE/Alu               ....A..T.C...........................
sf16                          .......T.C...........----------
sf48                          ....A..T.C...........----------
AluSq10#SINE/Alu              .......TTC...........................
sf80                          ....A..T.C...........----------
AluSp#SINE/Alu                ....A..T.C...........................
sf15_31                       ....A..T.C...........----------
sf33                          ....A..T.C...........----------
sf14                          ....A..T.C...........----------
sf32                          ....A..T.C...........----------
sf29                          .......T.C...........----------
AluSg#SINE/Alu                .......T.C...........................
AluSg4#SINE/Alu               .......T.C...........................
sf17                          .......T.C...........----------
AluSg7#SINE/Alu               .......T.C...........................
subfamily3_JB#SINE/Alu        .T.....T.......----------
subfamily4_Owl#SINE/Alu       .T.....T.C.....----------
subfamily20_JB#SINE/Alu       .T.....T.C.....----------
subfamily22_Owl#SINE/Alu      .T.....TTC.....----------
sf55                          .......T.C...........----------
sf34                          .......T.CA..........----------
AluSc#SINE/Alu                .......T.C...........................
sf64                          .......T.C...........----------
sf90                          .......T.C...........----------
sf3                           .......T.C...........----------
sf81                          .......T.C...........----------
```

```
sf54                        .......T.C..........----------
sf84                        .......T............----------
subfamily1_Ceb              .......T.C......----------
subfamily1_Owl#SINE/Alu     ..A....T.C......----------
subfamily38_JB#SINE/Alu     ..A....T.C.....----------
subfamily21_Owl#SINE/Alu    ..A....T.C......----------
subfamily35_JB#SINE/Alu     ..A....T.C.....----------
subfamily6_Ceb              ..A....T.C......----------
subfamily7_Owl#SINE/Alu     ..A....T.C......----------
subfamily14_Owl#SINE/Alu    ..A....T.C......----------
subfamily7_Ceb              ..A....T.C......----------
subfamily8_JB#SINE/Alu      ..A....T........----------
sf12                        .......T.C..........----------
subfamily26_Owl#SINE/Alu    ..A....T........----------
subfamily28_JB#SINE/Alu     ..A....T.C.....----------
subfamily13_Owl#SINE/Alu    ..A....T.C......----------
subfamily5_Owl#SINE/Alu     ..A....T.C......----------
subfamily12_Owl#SINE/Alu    ..A....T.C......----------
AluSc5#SINE/Alu             .......T.C.............................
sf35                        .......T.C..........----------
AluSc8#SINE/Alu             .......T.C.............................
AluTa7#SINE/Alu             .T.....T............----------
sf74                        .......T............----------
AluTa10#SINE/Alu            ....A..T.C..........----------
subfamily29_Owl#SINE/Alu    ....A..T.C.A....----------
sf69                        ....A..T.C..........----------
sf10                        ....A..T.C..........----------
sf39                        ....A..T.C..........----------
subfamily1_JB#SINE/Alu      ....A..T.C.....----------
subfamily11_JB#SINE/Alu     ....A..T.C.....----------
subfamily11_Owl#SINE/Alu    ....A..T.C......----------
subfamily23_JB#SINE/Alu     ....A..T.C.....----------
subfamily22_JB#SINE/Alu     ....A..T.C.....----------
sf61                        ....A..T.C..........----------
subfamily3_Owl#SINE/Alu     ....A..T.C......----------
subfamily41_JB#SINE/Alu     ....A..T.C...----------
subfamily16_Owl#SINE/Alu    ....A..T.C......----------
subfamily34_JB#SINE/Alu     ....A..T.C.....----------
subfamily6_JB#SINE/Alu      ....A..T.C.....----------
subfamily42_JB#SINE/Alu     ....A..T........----------
subfamily45_JB#SINE/Alu     ....A..T.C.....----------
subfamily33_JB#SINE/Alu     ....A..T.C.....----------
subfamily25_JB#SINE/Alu     ....A..T.C.....----------
subfamily44_JB#SINE/Alu     ....A..T.C.....----------
subfamily8_Owl#SINE/Alu     ....A..T.C......----------
subfamily31_JB#SINE/Alu     ....A..T.C.....----------
subfamily3_Ceb              ....A..T.C......----------
subfamily5_Ceb              ..A.A..T.C......----------
subfamily15_Owl#SINE/Alu    ....A..T.C......----------
subfamily7_JB#SINE/Alu      ....A..T.C.....----------
subfamily27_JB#SINE/Alu     ....A..T.C.....----------
subfamily21_JB#SINE/Alu     ....A..T.C.....----------
subfamily9_JB#SINE/Alu      ....A....C.....----------
subfamily26_JB#SINE/Alu     ....A....C.....----------
subfamily40_JB#SINE/Alu     ....A..T.C.....----------
subfamily17_JB#SINE/Alu     ....A..T.CA....----------
AluTa15#SINE/Alu            ....A..T.C..........----------
```

```
sf44                          ....A..T.C..........----------
subfamily0_JB#SINE/Alu        ....A..T.C.....----------
sf85                          ....A..T.C..........----------
sf86                          ....A..T.C..........----------
sf47                          ....A..T.C..........----------
sf63                          ....A..T.C.C........----------
sf73                          ....A..T.C..........----------
sf76                          ....A..T.C..........----------
subfamily18_JB#SINE/Alu       ....A..T.C.....----------
subfamily24_JB#SINE/Alu       ....A..T.C.....----------
subfamily20_Owl#SINE/Alu      ....A..T.C......----------
sf37                          ....A..T.C..........----------
sf38                          ....A..T.C..........----------
sf42                          ....A..T.C..........----------
sf46                          ....A..T.C..........----------
sf52                          ....A..T.C..........----------
sf53                          ....A..T.C..........----------
sf60                          ....A..T.C..........----------
sf62                          ....A..T.C..........----------
sf71                          ....A..T.C..........----------
sf82                          ....A..T.C...A......----------
subfamily18_Owl#SINE/Alu      ....A..T.C......----------
subfamily4_Ceb                ....A..T.C.A....----------
sf66                          ....A..T.C..........----------
sf36                          ....A..T.C..........----------
subfamily10_JB#SINE/Alu       ....A..T.C.....----------
subfamily29_JB#SINE/Alu       ....A..T.C.....----------
subfamily12_JB#SINE/Alu       ....A..T.CC....----------
subfamily19_JB#SINE/Alu       ....A..T.C.....----------
subfamily10_Owl#SINE/Alu      ....A..T.C......----------
subfamily17_Owl#SINE/Alu      ....A..T.C......----------
subfamily23_Owl#SINE/Alu      ....A..T.C......----------
sf11                          ....A..T.C..........----------
sf4                           ....A..T.C..........----------
sf51                          ....A..T.C..........----------
subfamily25_Owl#SINE/Alu      ....A..T.C......----------
subfamily5_JB#SINE/Alu        ....A..T.C.....----------
subfamily24_Owl#SINE/Alu      ....A..T.C......----------
subfamily37_JB#SINE/Alu       ....A..T.C.....----------
subfamily39_JB#SINE/Alu       ....A..T.C.....----------
subfamily19_Owl#SINE/Alu      .......T.C......----------
subfamily2_Ceb                ....A..T.C......----------
subfamily8_Ceb                .G..A..T.C......----------
subfamily14_JB#SINE/Alu       ..A.A..T.C.....----------
subfamily4_JB#SINE/Alu        ....A..T.C.....----------
subfamily9_Owl#SINE/Alu       .......T.C......----------
sf65                          ....A..T.C..........----------
subfamily16_JB#SINE/Alu       ....A..T.C.....----------
subfamily2_JB#SINE/Alu        ....A..T.C.....----------
subfamily43_JB#SINE/Alu       ....A..T.C.....----------
subfamily30_JB#SINE/Alu       ....A..T.C.....----------
subfamily15_JB#SINE/Alu       ....A..T.C.....----------
subfamily36_JB#SINE/Alu       ....A..T.C.....----------
sf5                           ....A..T.C..........----------
sf43                          ....A..T.C..........----------
subfamily32_JB#SINE/Alu       ....A..T.C.....----------
subfamily13_JB#SINE/Alu       ....A..T.C.....----------
```

Figure A4.2: Alignment of all 189 *Alu* subfamilies used to generate a network and Bayesian phylogenetic tree. Dots represent a shared nucleotide while diagnostic substitutions are shown as the corrected base compared to the *Alu*Jb subfamily.

Table A4.3. RepeatMasker summary and removal of subfamily duplicates. Grey highlights RepBase (Jurka et al. 2005) or Ray and Batzer 2005 subfamilies; green, purple, blue and orange highlight the lineage-specific subfamilies from the marmoset, squirrel monkey, owl monkey and capuchin monkey genomes, respectively. Red highlighted subfamilies have been removed as duplicates.

Original designation	RepeatMasker subgroup
AluJb	Jb
sf9	Jb
sf22	Jb
sf24	Jb
sf56	Jb
sf78	Jb
sf87	Jb
sf88	Jb
sf92	Jb
AluJo	Jo
sf2	Jo
sf21	Jo
sf57	Jo
sf89	Jo
AluJr	Jr
sf23	Jr
sf40	Jr
sf41	Jr
sf45	Jr
sf58	Jr

sf67	Jr
sf68	Jr
sf70	Jr
sf79	Jr
sf83	Jr
AluJr4	Jr4
AluSc	Sc
subfamily8_jb	Sc
subfamily28_jb	Sc
subfamily35_jb	Sc
subfamily38_jb	Sc
subfamily1_Ceb	Sc
subfamily6_Ceb	Sc
subfamily7_Ceb	Sc
subfamily1_Owl	Sc
subfamily5_Owl	Sc
subfamily7_Owl	Sc
subfamily12_Owl	Sc
subfamily13_Owl	Sc
subfamily14_Owl	Sc
subfamily21_Owl	Sc
subfamily26_Owl	Sc
sf3	Sc
sf12	Sc
sf54	Sc
sf64	Sc
sf81	Sc
sf84	Sc
sf90	Sc
AluSc5	Sc5
AluSc8	Sc8
sf35	Sc8
AluSg	Sg
subfamily20_jb	Sg
subfamily22_Owl	Sg
sf18	Sg
sf34	Sg
AluSg4	Sg4
subfamily3_jb	Sg4
subfamily4_Owl	Sg4
AluSg7	Sg7

sf17	Sg7
sf55	Sg7
AluSp	Sp
sf15_31	Sp
sf72	Sp
AluSq	Sq
sf32	Sq
AluSq10	Sq10
AluSq2	Sq2
sf14	Sq2
sf16	Sq2
sf29	Sq2
sf33	Sq2
sf80	Sq2
AluSq4	Sq4
AluSx	Sx
sf8	Sx
sf26	Sx
sf30	Sx
sf75	Sx
sf93	Sx
AluSx1	Sx1
sf19	Sx1
sf48	Sx1
sf59	Sx1
AluSx3	Sx3
sf91	Sx3
AluSx4	Sx4
AluSz	Sz
sf7	Sz
sf77	Sz
AluSz6	Sz6
sf25	Sz6
sf28	Sz6
sf50	Sz6
AluTa10	Ta10
subfamily1_jb	Ta10
subfamily6_jb	Ta10
subfamily7_jb	Ta10
subfamily9_jb	Ta10
subfamily11_jb	Ta10

subfamily17_jb	Ta10
subfamily21_jb	Ta10
subfamily22_jb	Ta10
subfamily23_jb	Ta10
subfamily25_jb	Ta10
subfamily26_jb	Ta10
subfamily27_jb	Ta10
subfamily31_jb	Ta10
subfamily33_jb	Ta10
subfamily34_jb	Ta10
subfamily40_jb	Ta10
subfamily41_jb	Ta10
subfamily42_jb	Ta10
subfamily44_jb	Ta10
subfamily45_jb	Ta10
subfamily3_Ceb	Ta10
subfamily5_Ceb	Ta10
subfamily3_Owl	Ta10
subfamily8_Owl	Ta10
subfamily11_Owl	Ta10
subfamily15_Owl	Ta10
subfamily16_Owl	Ta10
subfamily29_Owl	Ta10
sf10	Ta10
sf39	Ta10
sf61	Ta10
sf69	Ta10
AluTa15	Ta15
subfamily0_jb	Ta15
subfamily2_jb	Ta15
subfamily4_jb	Ta15
subfamily5_jb	Ta15
subfamily10_jb	Ta15
subfamily12_jb	Ta15
subfamily13_jb	Ta15
subfamily14_jb	Ta15
subfamily15_jb	Ta15
subfamily16_jb	Ta15
subfamily18_jb	Ta15
subfamily19_jb	Ta15
subfamily24_jb	Ta15

subfamily29_jb	Ta15
subfamily30_jb	Ta15
subfamily32_jb	Ta15
subfamily36_jb	Ta15
subfamily37_jb	Ta15
subfamily39_jb	Ta15
subfamily43_jb	Ta15
subfamily2_Ceb	Ta15
subfamily4_Ceb	Ta15
subfamily8_Ceb	Ta15
subfamily9_Owl	Ta15
subfamily10_Owl	Ta15
subfamily17_Owl	Ta15
subfamily18_Owl	Ta15
subfamily19_Owl	Ta15
subfamily20_Owl	Ta15
subfamily23_Owl	Ta15
subfamily24_Owl	Ta15
subfamily25_Owl	Ta15
sf4	Ta15
sf5	Ta15
sf11	Ta15
sf36	Ta15
sf37	Ta15
sf38	Ta15
sf42	Ta15
sf43	Ta15
sf44	Ta15
sf46	Ta15
sf47	Ta15
sf51	Ta15
sf52	Ta15
sf53	Ta15
sf60	Ta15
sf62	Ta15
sf63	Ta15
sf65	Ta15
sf66	Ta15
sf71	Ta15
sf73	Ta15
sf76	Ta15

sf82	Ta15
sf85	Ta15
sf86	Ta15
AluTa7	Ta7
sf74	Ta7
AluJr_sf6	Same as AluJr
AluSq2_sf13	Same as AluSq2
subfamily0_Owl	Same as AluTa15
subfamily27_Owl	Same as sf63
subfamily2_Owl	Same as subfamily0_JB
subfamily28_Owl	Same as subfamily2_Owl
subfamily6_Owl	Same as subfamily6_JB
subfamily0_Ceb	Same as subfamiy0_JB

Appendix B. Letter of Permission

From: Jessica Storer [mailto:jstore5@lsu.edu]
Sent: 23 August 2019 17:28
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Thank you for your help.

Sincerely,

Jessica Storer, MS
PhD Student
Batzer Laboratory of Comparative Genomics
https://biosci-batzerlab.biology.lsu.edu/

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Louisiana State University
Baton Rouge, LA, 70803

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To: Jessica Storer <jstore5@lsu.edu>

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Dear Jessica Storer,

RE. Jessica M Storer, Jackson R Mierl, Sarah A Brantley et al. Amplification dynamics of Platy-1 retrotransposons in the Cebidae Platyrrhine lineage. *Genome Biology and Evolution* (2019) 11 (4): 1105-1116, 10.1093/gbe/evz062

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Vita

Jessica Marie Storer was born in Norwalk, Ohio to two proud parents, Hugh Storer and Therese Storer, joining a sibling, Meagan Grauel, then Meagan Storer. She grew up in Norwalk before heading to college at Providence College in Providence, Rhode Island in 2007 after graduating top of her class at St. Paul's Catholic High School. She then pursued a Master's degree in Molecular, Cellular and Developmental Biology studying plant viruses at The Ohio State University before heading down to Louisiana State University to earn her Doctorate degree under the tutelage of Dr. Mark Batzer. She will continue on the path that her Doctoral degree has taken her by joining Dr. Arian Smit and associates in Seattle, Washington at the Insitute for Systems Biology to continue to study mobile elements.